

ude of CTL responses are shown as follows: + up to 2 LU (Lytic Units) or 10 SV (Secretory Units); ++ up to 200 LU or 100 SU; +++ up to 200 LU or 100 SU; ++++more than 200 LU or 1000 SU. Magnitude represents number of independent cultures yielding positive responses.

cognition	++	-	++	++	++	++
frequency	7/13	0/8	10/14	18/19	9/11	4/13
						-
						0/19
						5/8

NS4 1812	CORE 132	NS4 1590	NS4 1851	NS4 2611	NS4 1769	CORE 35	5	16	2	NS1/E2 728	22	7	23 1883/ 18 64	NS4	CORE 51	NS3 1396	2	14	NS1/E 2 632	ENVI 290	CORE 43	25	PADRE
A2	A2	A2	A2	A2	A2	A2	A2	A2	A2	A2	A2	A1	A1	A3	B7	A3	A24	B7	A3	A3	A3	A31	
++	+++	++	-	-	++	++				-				++		+			+	+	+	+	
1/12	2/12	5/12	0/12	0/12	2/12	6/12				0/12				5/6		4/6	1/6		2/6	1/6	0/6		

magnitude	++	+++	+	-	-	++	++
frequency	1/12	2/12	5/12	0/12	0/12	2/12	6/12

magnitude	+++	++ +	+++	++	++ ++ ++	+	-	+++	++	+
frequency	17/18	6/6 1/9	12/12	14/18	4/18 4/18 9/9	1/9	0/6	6/6	1/6 1/6	6/12 :

1/90

FIG. 1

2/90

Synthetic polypeptides encoding HIV-derived HTL epitopes

HIV pol 711	HIV gag 171	HIV pol 335	HIV pol 303
-------------	-------------	-------------	-------------

HTL polypeptide



functional peptides*

HIV pol 711	<u>GPGPG</u>	HIV gag 171	<u>GPGPG</u>	HIV pol 335	<u>GPGPG</u>	HIV pol 303
-------------	--------------	-------------	--------------	-------------	--------------	-------------

spacer optimized polypeptide

Epitope peptides comprise either 10 amino acids from the N-terminal epitope and 5 amino acids from the C-terminal epitope or 5 amino acids from the N-terminal epitope and 10 amino acids from the C-terminal epitope.

FIG. 2A

Proliferative responses to synthetic polypeptides encoding HIV-derived HTL

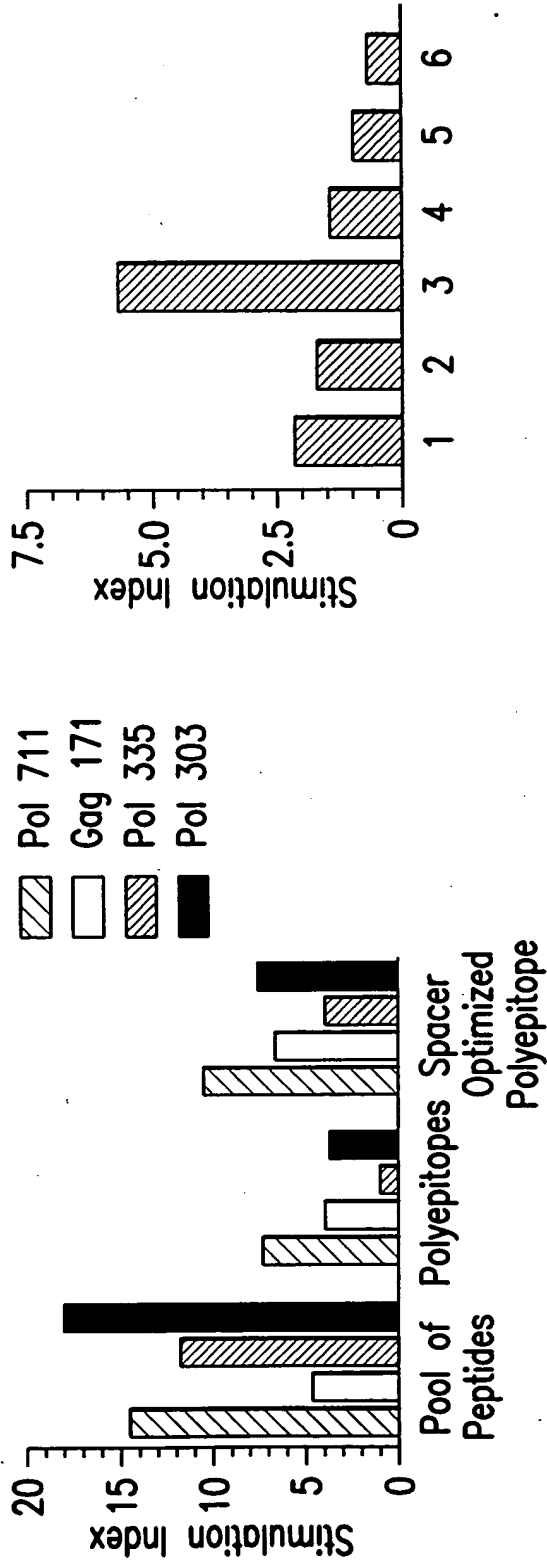


FIG.2B

4/90

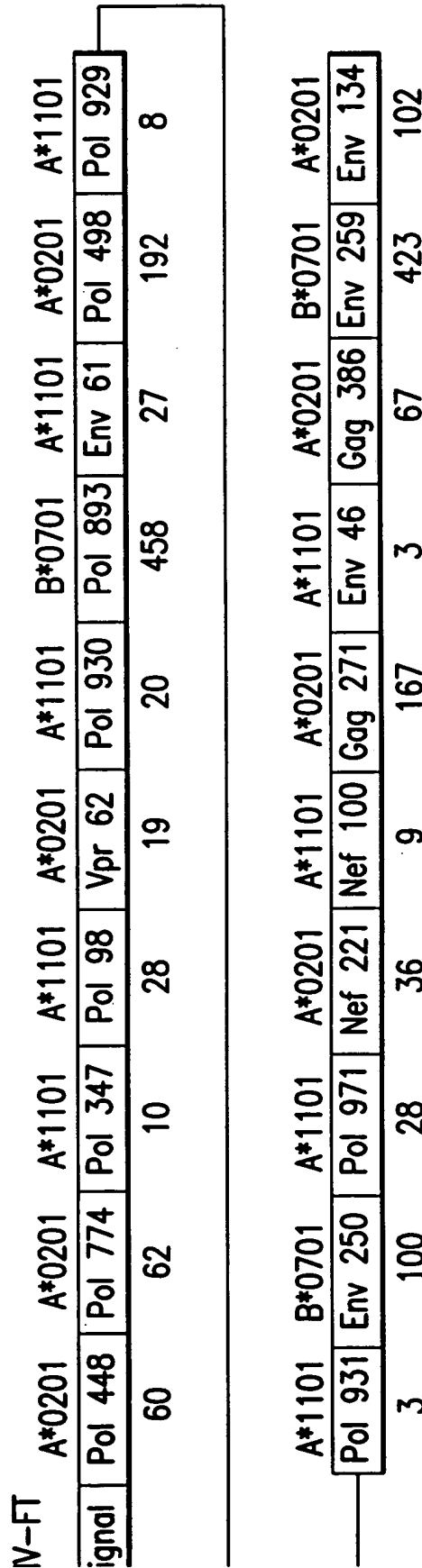


FIG.3A

5/90

--specific multiepitope constructs

1

A*1101

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*1101

A*1101

A*0201

14

pol 149

PADRE®

core 18

pol 562

pol 551

pol 455

env 183

core 141

pol 665

env 335

2

↑

8

5

76

10

4

11

5

F↓

2

A*1101

A*0201

A*1101

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*1101

A*1101

A*1101

A*0201

14

pol 149

PADRE®

core 18

pol 629

pol 562

pol 551

pol 455

env 183

core 141

pol 665

env 335

2

↑

353

8

76

10

4

11

5

K↓

1X

A*1101

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*0201

A*1101

A*1101

A*1101

A*0201

14

pol 149

PADRE®

core 18

C1

pol 562

pol 551

pol 455

env 183

core 141

pol 665

env 335

2

↑

353

8

76

10

4

11

5

K↓

C1 = either W, Y, L, K, R, C, N or G

FIG.3B

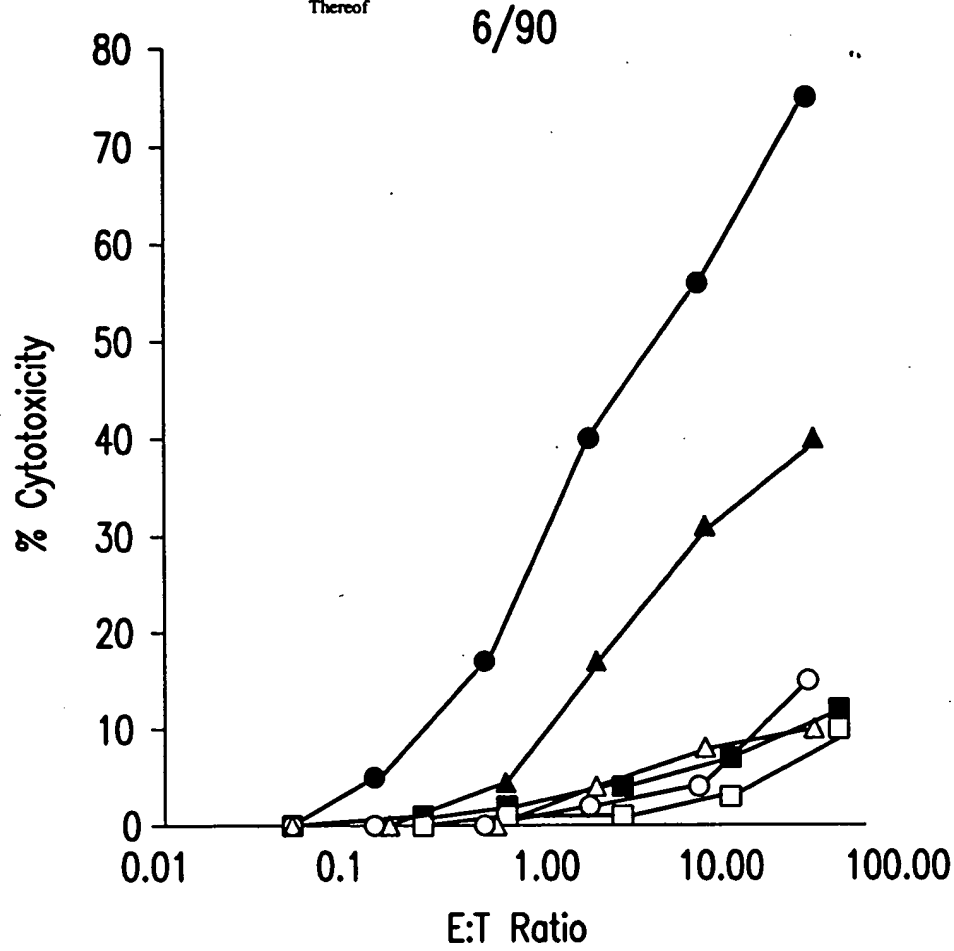
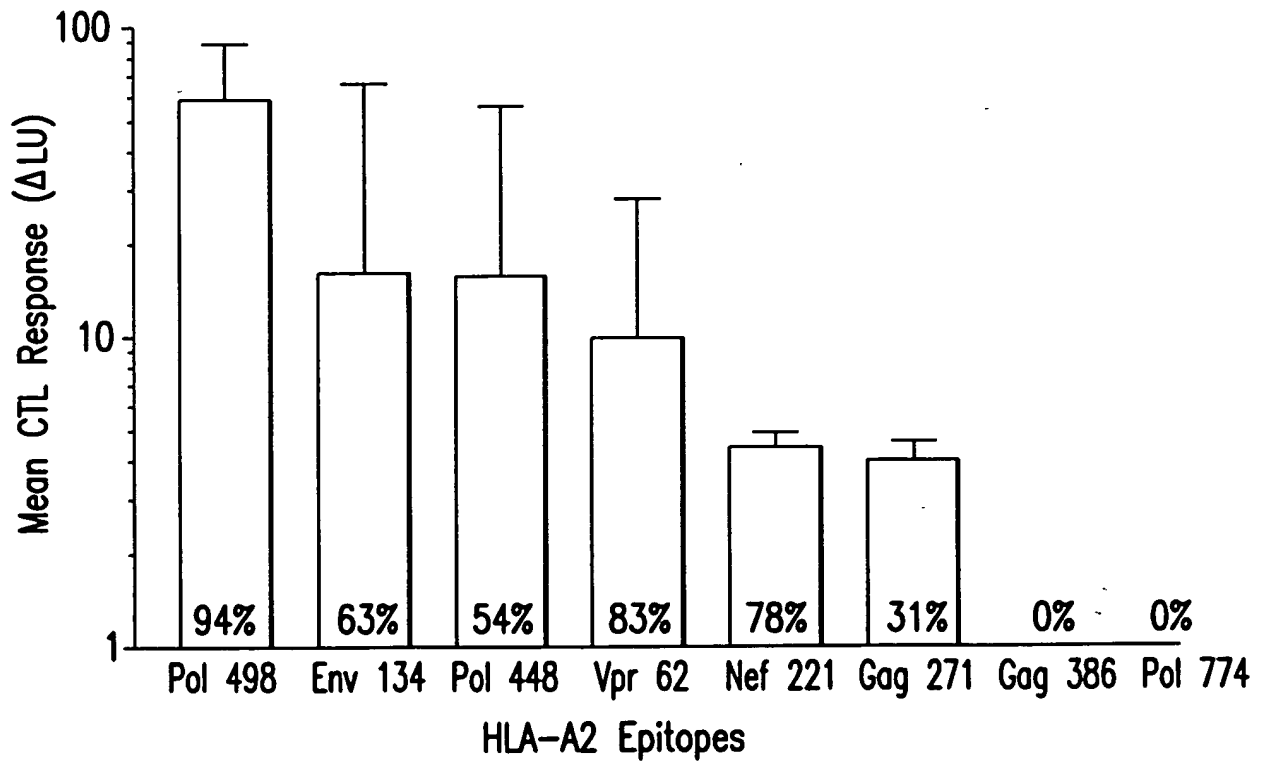


FIG. 4A



7/90

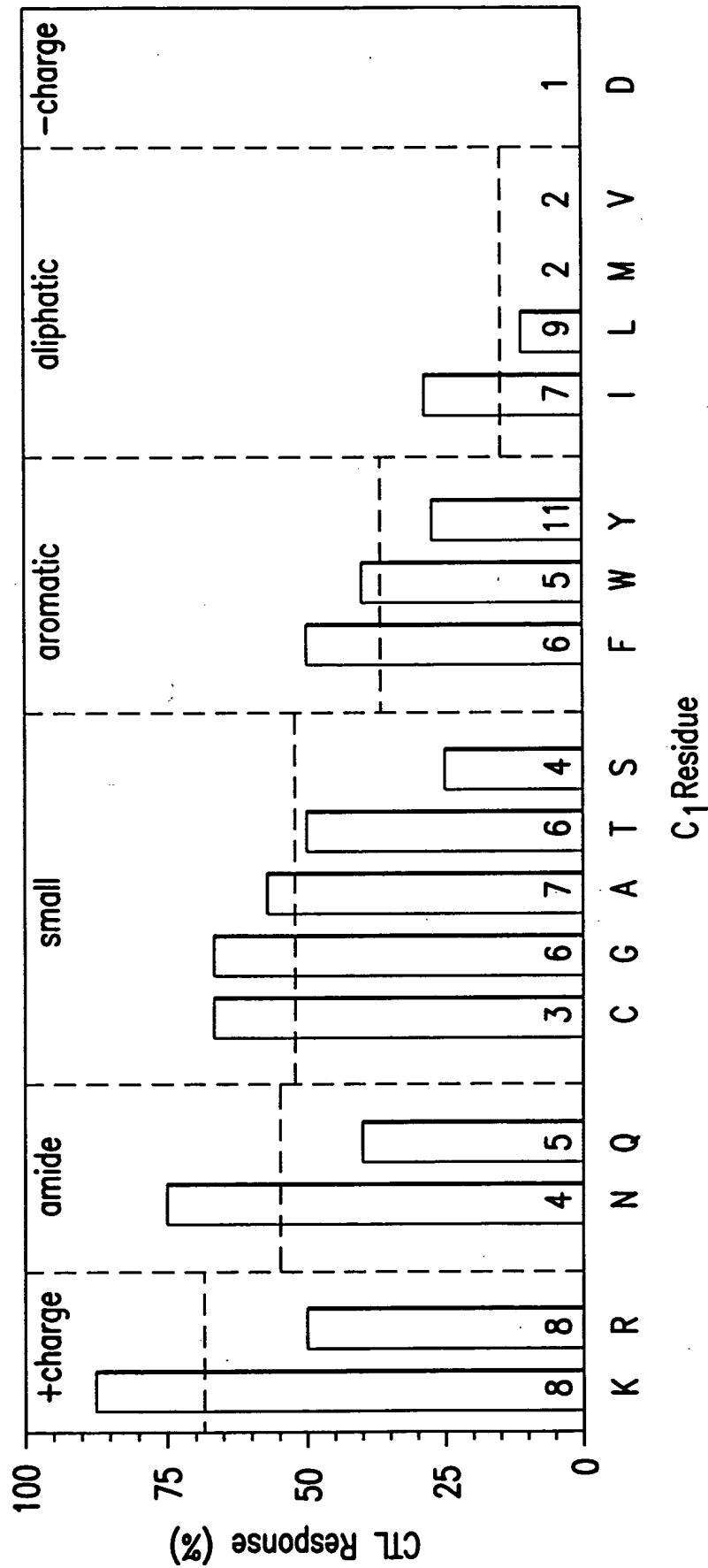


FIG.5

8/90

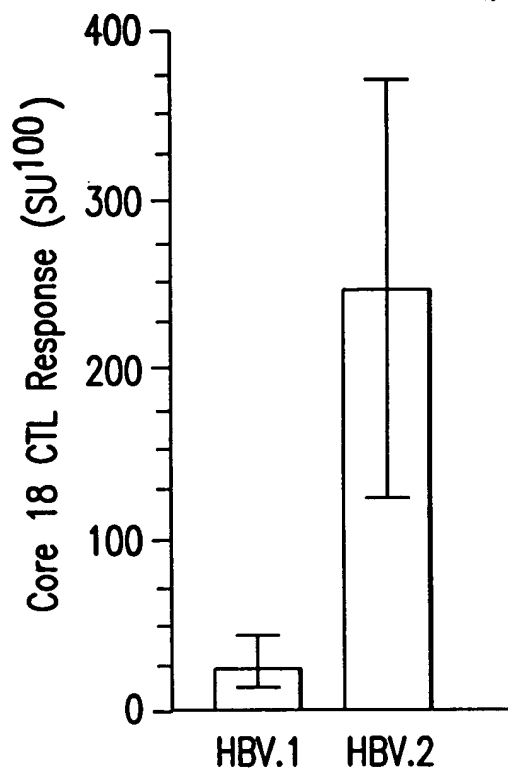
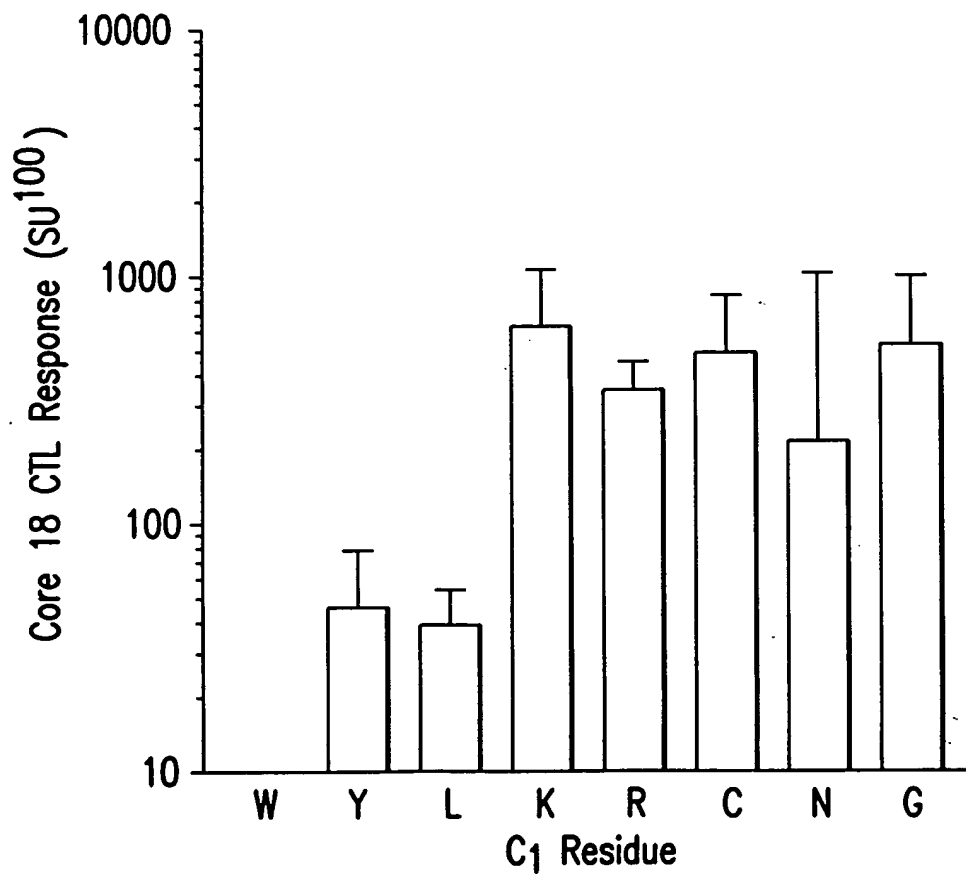


FIG.6A



9/90

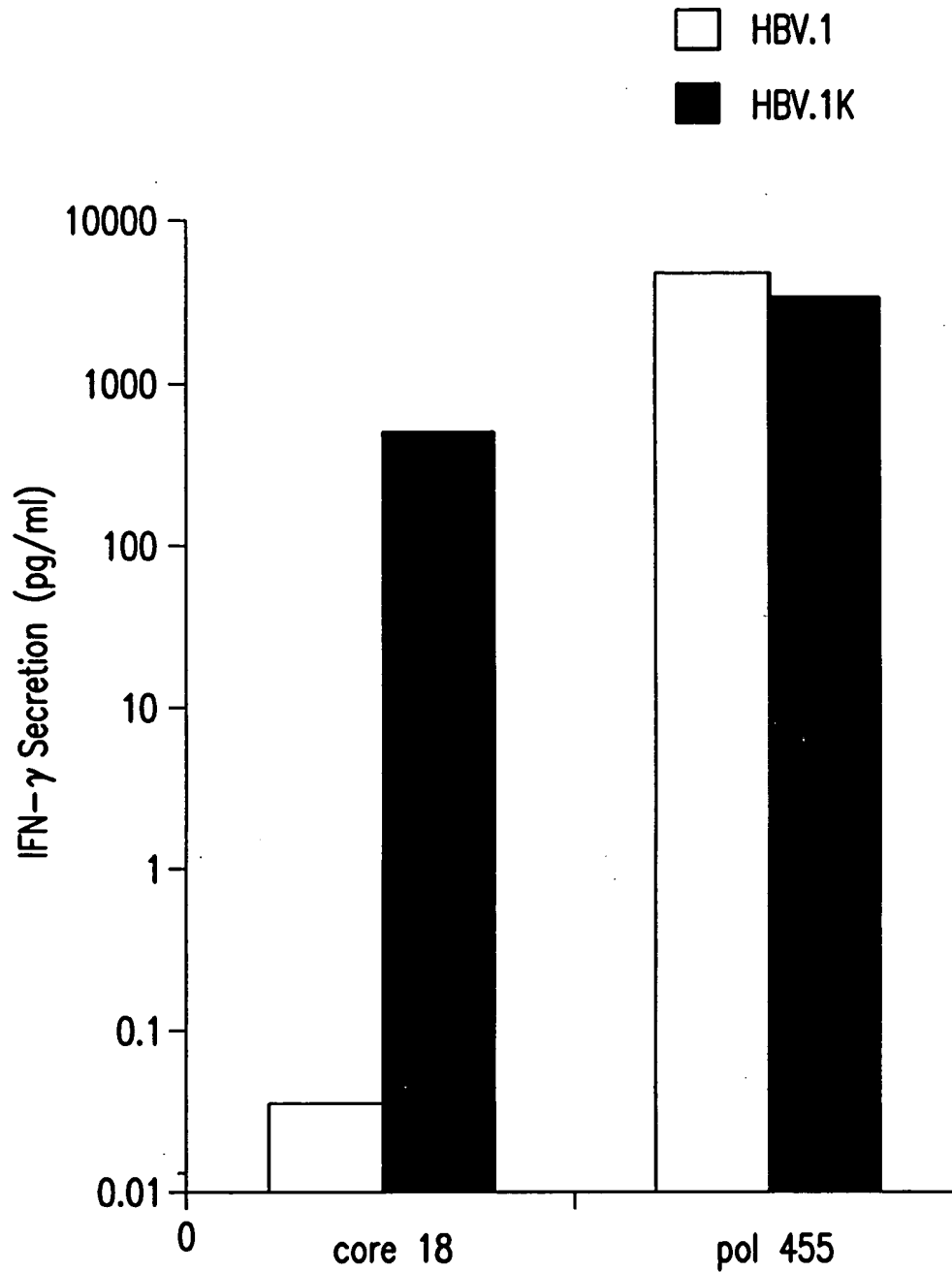
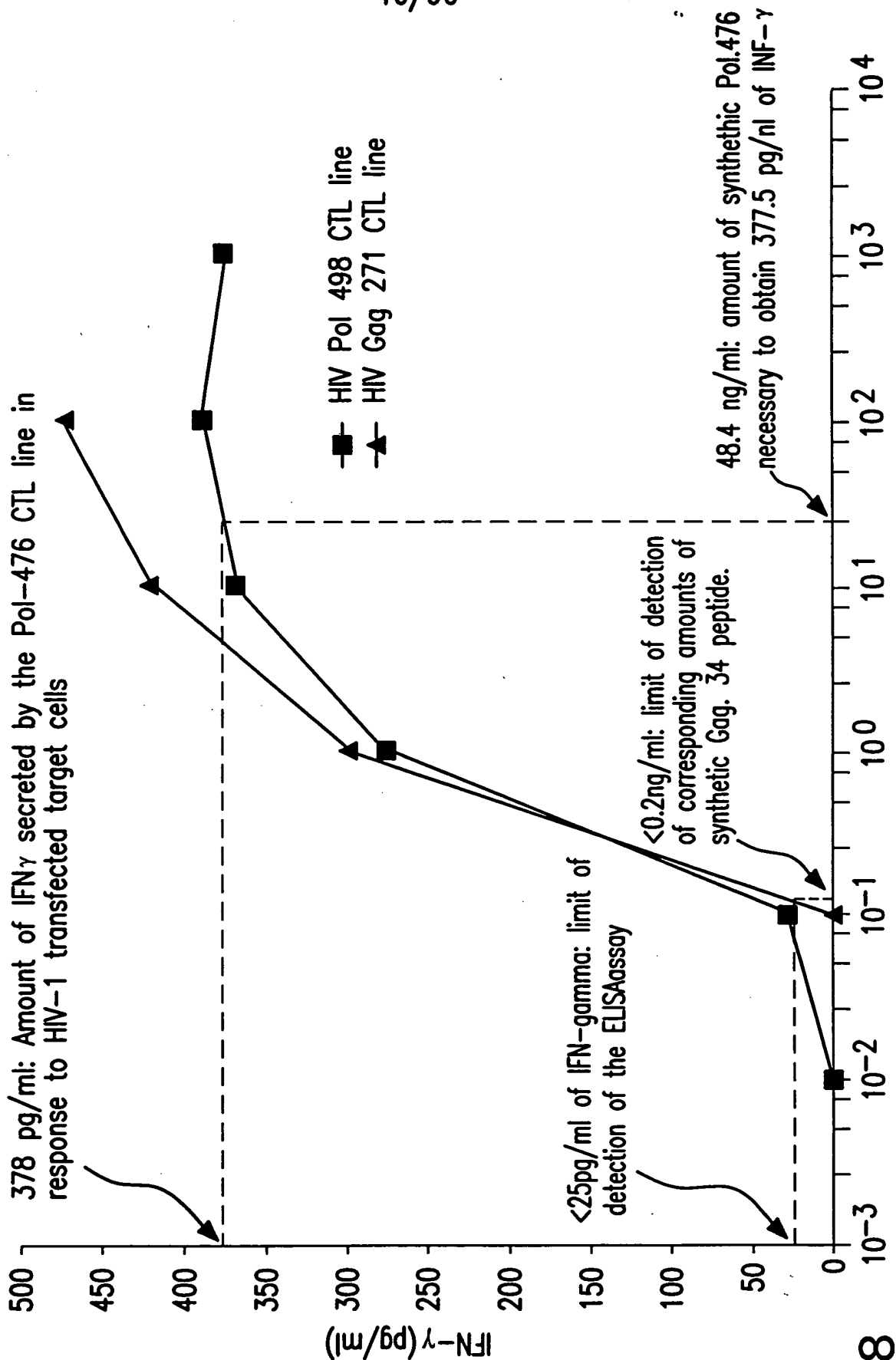


FIG.7

10/90

Antigenicity assays as a way to measure epitope production in minigene-transfected cells.



11/90

> HIV-1090

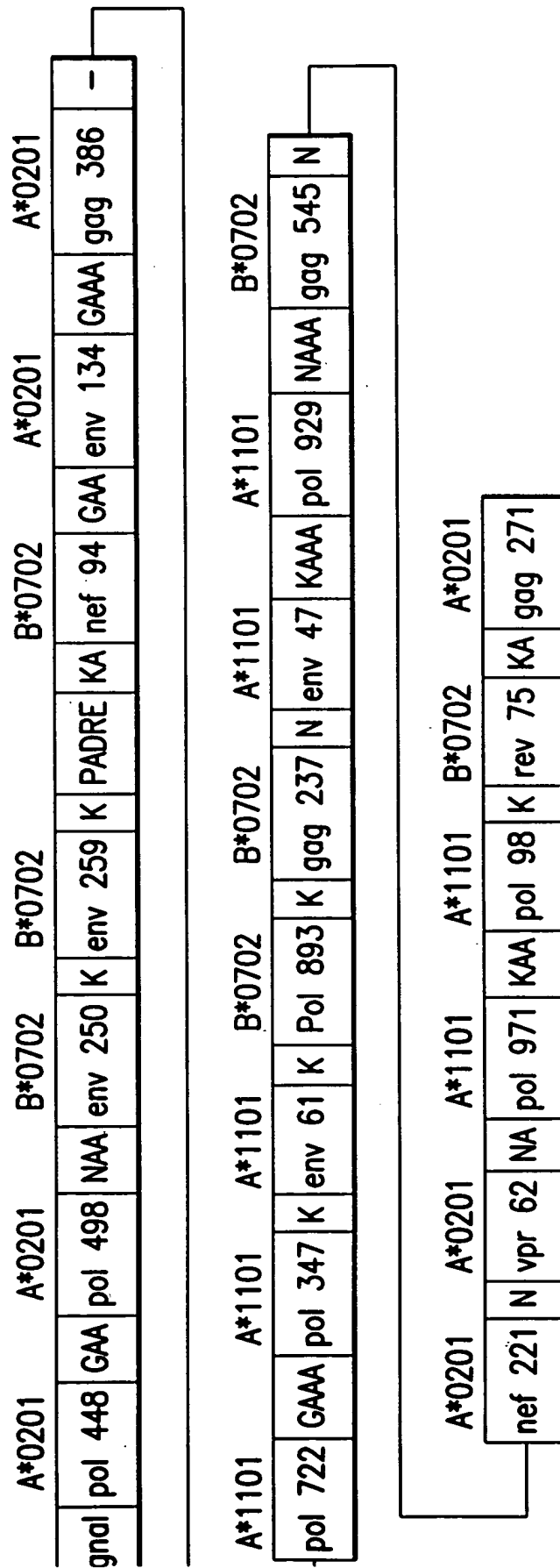


FIG. 9A

12/90

-CPT

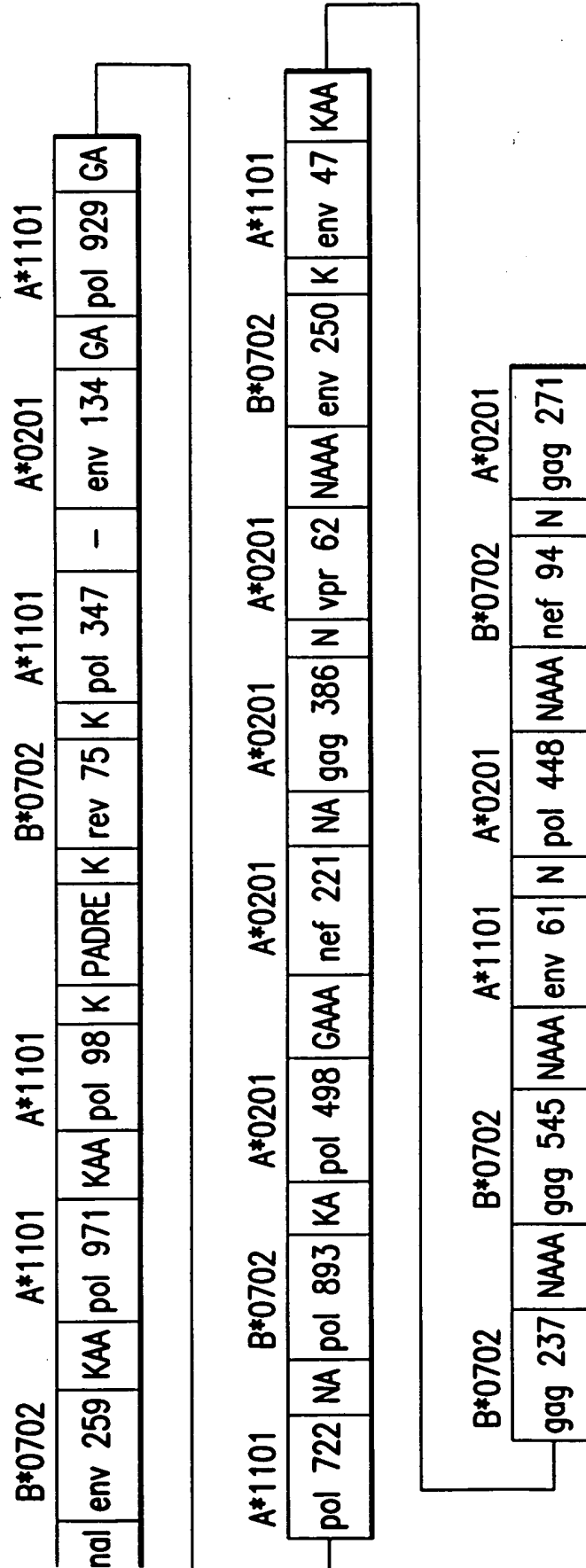
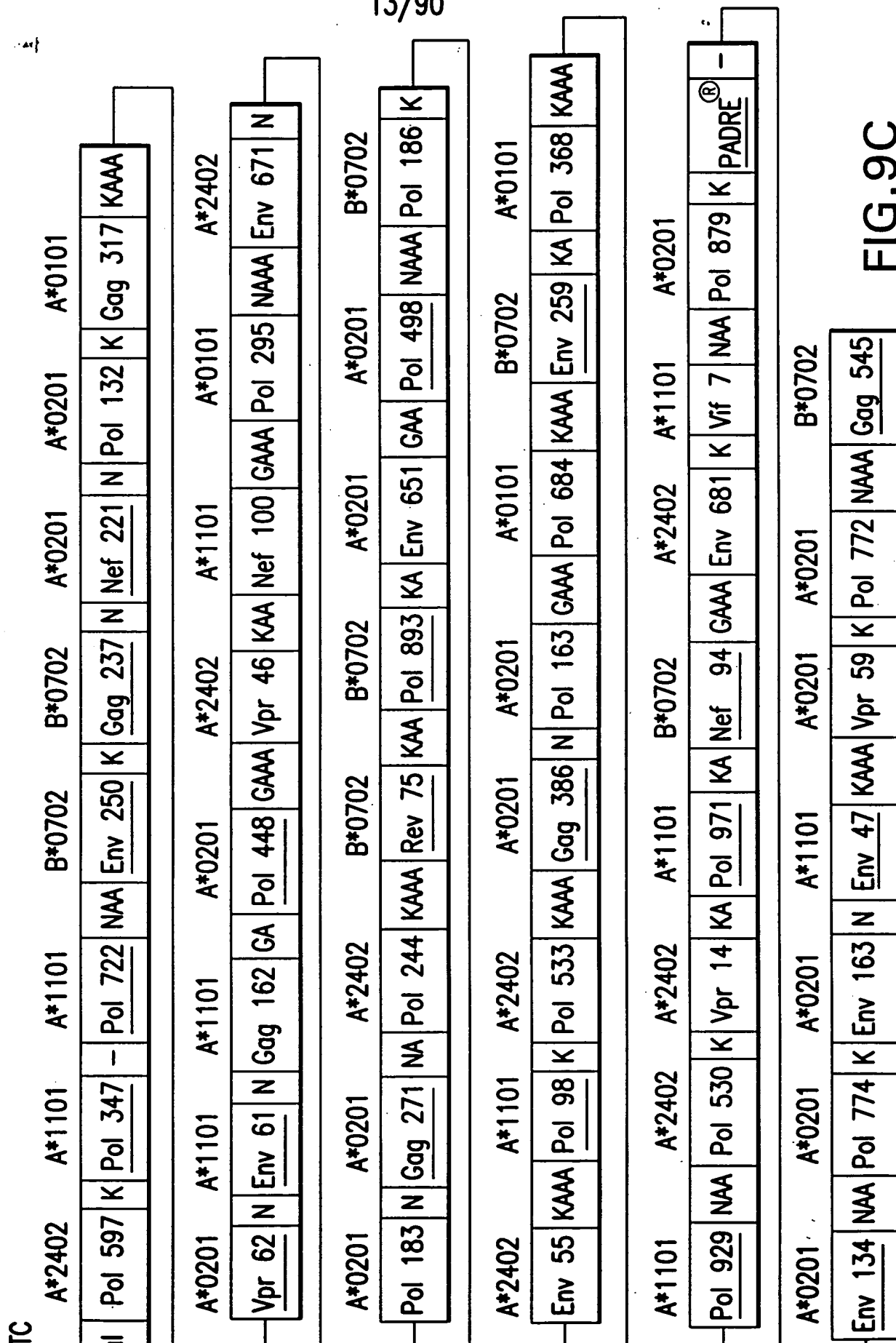


FIG. 9B

13/90



14/90

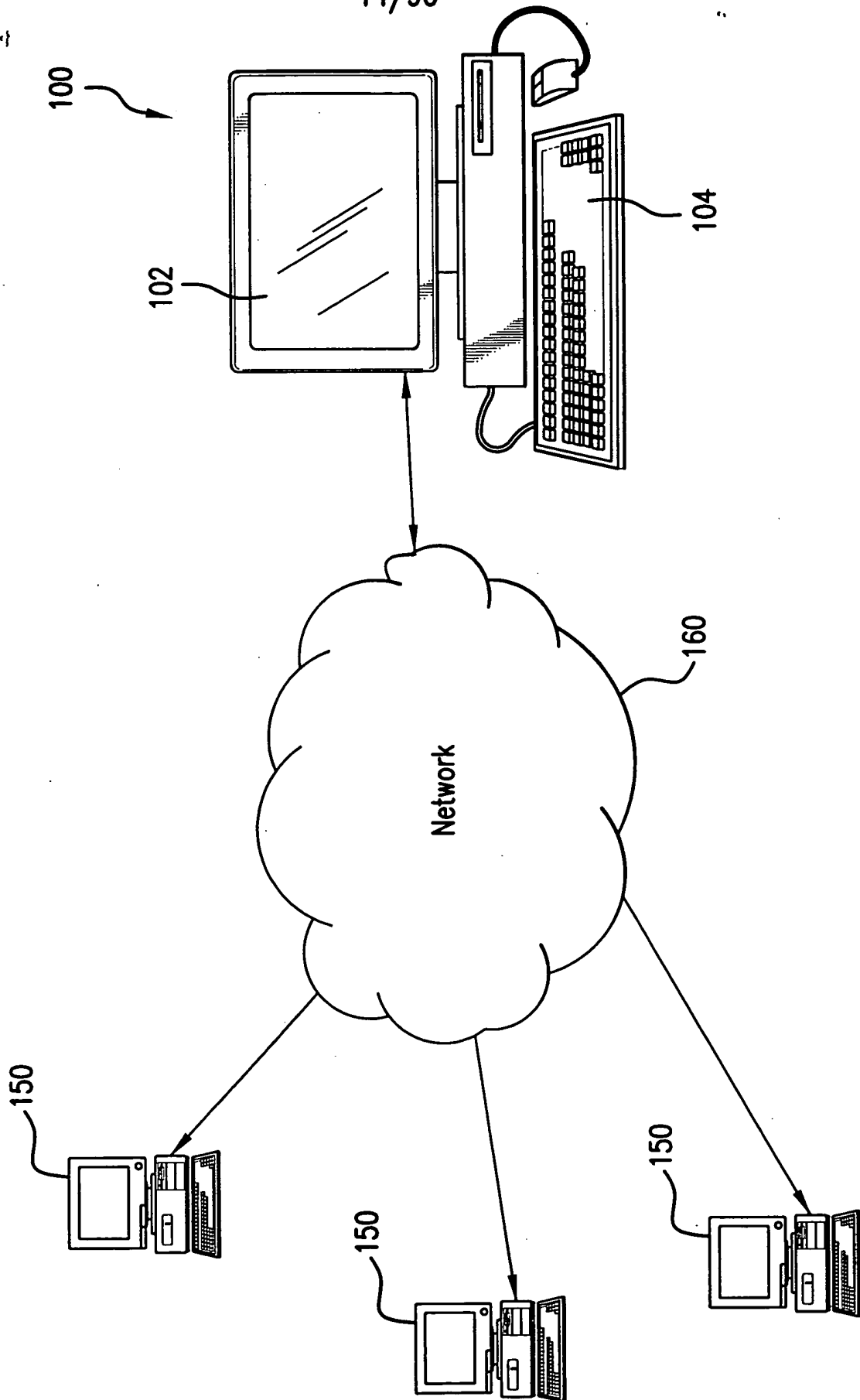


FIG. 10

Sequence	Length	Code
VLAEMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFIHNFK	10	E
VTVYYGVPVWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VIYQYMDDL Y	10	I
IYQEPFKNL	9	J
IWGCSGKLI	9	K

200
 202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LIMV)
 XXXX(FY)XXX(LIMV)
 XXXXNXXX(LIMV)
 XXXXNXXX(LIMV)
 X(LM)XXXXXXV
 X(LM)XXXXXXV
 X(LMVT)XXXXXX(KRY)
 X(LMVT)XXXXXX(KRY)

206

MaxInsertions={enter value here} 208

OutputToScreen=yes/no 210

OutputToFile=yes/no 212

MinimumAccepted={enter value here} 214

MaxDuplicateFunctionValues={enter value here} 216

MaxSearchTime (min.)={enter value here} 218

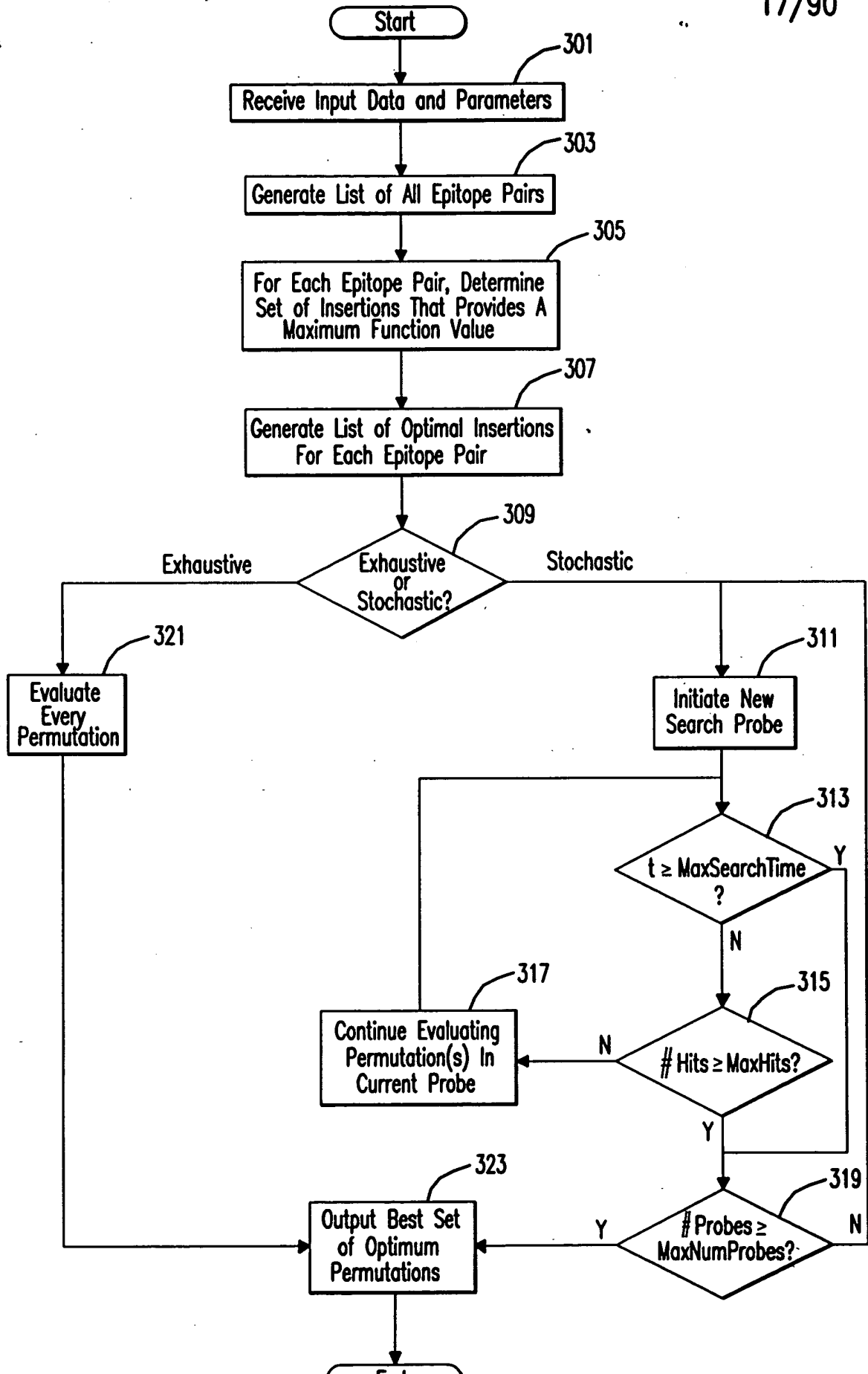
Exhaustive=yes/no 220

NumStochasticProbes={enter value here} 222

MaxHitsPerProbe={enter value here} 224

RandomProbeStart=yes/no 226

FIG. 11B



Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm. 18/90

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count Motif Specification

1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAAMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIAV	10
E	QMAVF IHNFK	10
F	VTVYYGVPVWK	11
G	FPVRPQVPL	9
H	YPLASLRSLF	10
I	VIYQYMDLY	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

19/90

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A	A	R	C	2.00	1.57	3.14	0	6.28
B	C	A	A	R	D	2.00	1.57	3.14	0	6.28
B	C	A	A	R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	R	F	2.00	1.33	2.66	1	2.66
B	C		A	G	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C			R	B	2.00	1.57	3.14	1	3.14
C	C	A		L	D	2.00	2.20	4.40	1	4.40
C	C			R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C			R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIG.13B

20/90

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
DD	CC			LL	AB	2.00	2.20	4.40	0	8.80
DDD	CCC			LLL	CEF	2.00	2.20	4.40	0	8.80
DDDD	CCCC			LLLL	FGH	2.00	2.20	4.40	0	8.80
DDDD	CCCC			RR	GH	1.80	1.33	2.39	0	4.79
DDDD	CCCC	A	A	RGL	HI	2.00	1.57	3.14	0	6.28
DDDD	CCCC	A		GL	IJ	2.00	1.33	2.66	0	5.32
DDDD	CCCC	A		LR	JK	2.00	2.20	4.40	1	4.40
DDDE	CCCC	A		RL	AB	2.00	1.33	2.66	0	5.32
DDDE	CCCC	A	A	LL	BC	2.00	1.57	3.14	0	6.28
DDDE	CCCC	A	A	LL	CD	2.00	2.20	4.40	0	8.80
DDDE	CCCC	A	A	LL	DE	2.00	2.20	4.40	0	8.80
DDDE	CCCC	A	A	LL	FG	2.00	2.20	4.40	0	8.80
DDDE	CCCC	A	A	RR	GH	2.00	1.57	3.14	0	6.28
DDDE	CCCC	A		RR	HI	2.00	1.57	3.14	0	6.28
DDDE	CCCC	A	A	RR	IJ	2.00	2.20	4.40	0	8.80
DDDE	CCCC	A		RL	JK	2.00	1.57	3.14	0	6.28
DDDE	CCCC	A		RL	AB	2.00	1.57	3.14	0	6.28
DDDE	CCCC	A	A	RL	BC	2.20	2.20	4.84	1	4.84
DDDE	CCCC	A	A	GG	CD	2.20	1.33	2.93	1	2.93
DDDE	CCCC	A	A	GG	DE	2.20	1.33	2.93	0	5.85
DDDE	CCCC	A	A	GG	EH	2.20	1.33	2.93	0	5.85
DDDE	CCCC	A		GG	GH	2.20	1.33	2.93	1	2.93
DDDE	CCCC	A	A	GG	HI	2.20	1.33	2.93	1	2.93
DDDE	CCCC	A		GR	IJ	2.20	1.57	3.45	1	3.45
DDDE	CCCC	A		RR	JK	2.20	1.57	3.45	0	6.91
DDDE	CCCC	AA		RR	AB	2.00	1.57	3.14	1	3.14
DDDE	CCCC	AA		RR	BC	2.00	1.57	3.14	2	1.57
DDDE	CCCC	AA		RR	CD	2.00	1.57	3.14	1	3.14
DDDE	CCCC	A		RL	DE	2.00	2.20	4.40	1	4.40
DDDE	CCCC			LL	EF	2.00	1.57	3.14	2	1.57
DDDE	CCCC			LL	FG	2.00	2.20	4.40	4	1.10
DDDE	CCCC			GR	HI	2.00	1.33	2.66	0	5.32
DDDE	CCCC	AA	A	RR	IJ	2.00	1.57	3.14	2	1.57
DDDE	CCCC	AA	A	RR	JK	2.00	1.57	3.14	1	3.14
DDDE	CCCC	AA	A	RR	AB	2.00	1.57	3.14	0	6.28
DDDE	CCCC	AA	A	GG	BC	2.00	1.33	2.66	0	5.32
DDDE	CCCC	AA	A	GG	CD	2.00	1.33	2.66	1	2.66
DDDE	CCCC	AA	A	GG	DE	2.00	1.33	2.66	0	5.32
DDDE	CCCC	AA	A	GG	EF	2.00	1.33	2.66	0	5.32
DDDE	CCCC	AA	A	GG	FG	2.00	1.33	2.66	0	5.32
DDDE	CCCC	AA	A	GG	GH	2.00	1.57	3.14	1	2.66
DDDE	CCCC	AA	A	GG	HI	2.00	1.33	2.66	1	2.66
DDDE	CCCC	AA	A	GG	IJ	2.00	1.33	2.66	1	2.66
DDDE	CCCC	AA	A	GG	JK	2.00	1.33	2.66	0	5.32

FIG.13C

21/90

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K		A	R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A	A	G	J	2.20	1.33	2.93	1	2.93
I	K	A	A	G	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A	A	R	C	2.20	1.57	3.45	0	6.91
J	K	A	A	R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K	A	A	R	F	2.20	1.57	3.45	2	1.73
J	K		A	R	G	2.20	1.57	3.45	1	3.45
J	K			R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
J	K	A	A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	1.57	3.45	1	3.45
K	G				G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			L	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIG.13D

22/90

CTL responses induced by EP HIV-1090 relative to individual peptides in IFA

▨ Peptide/IFA
 ■ EP HIV-1090

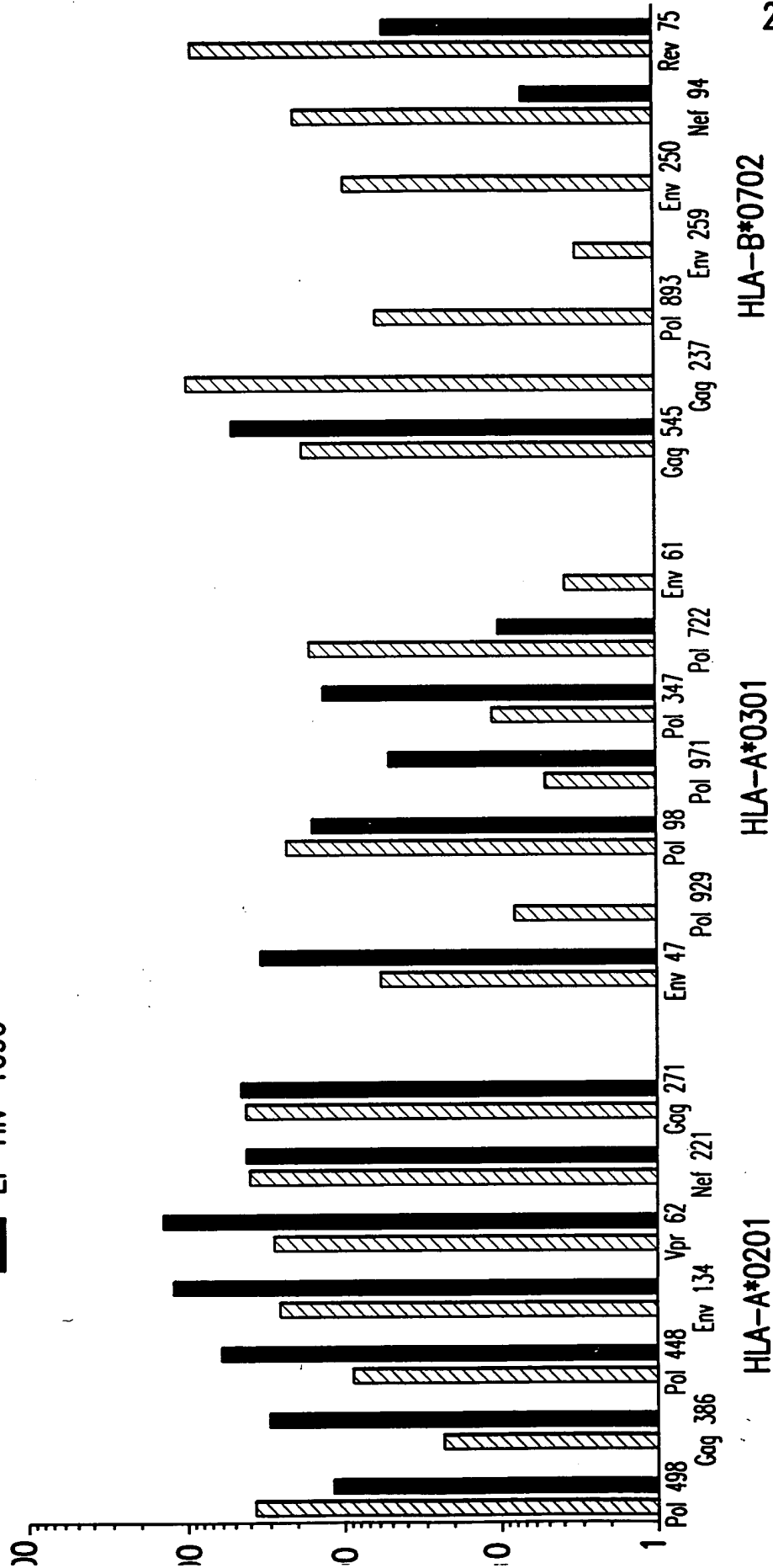


FIG. 14A

23/90

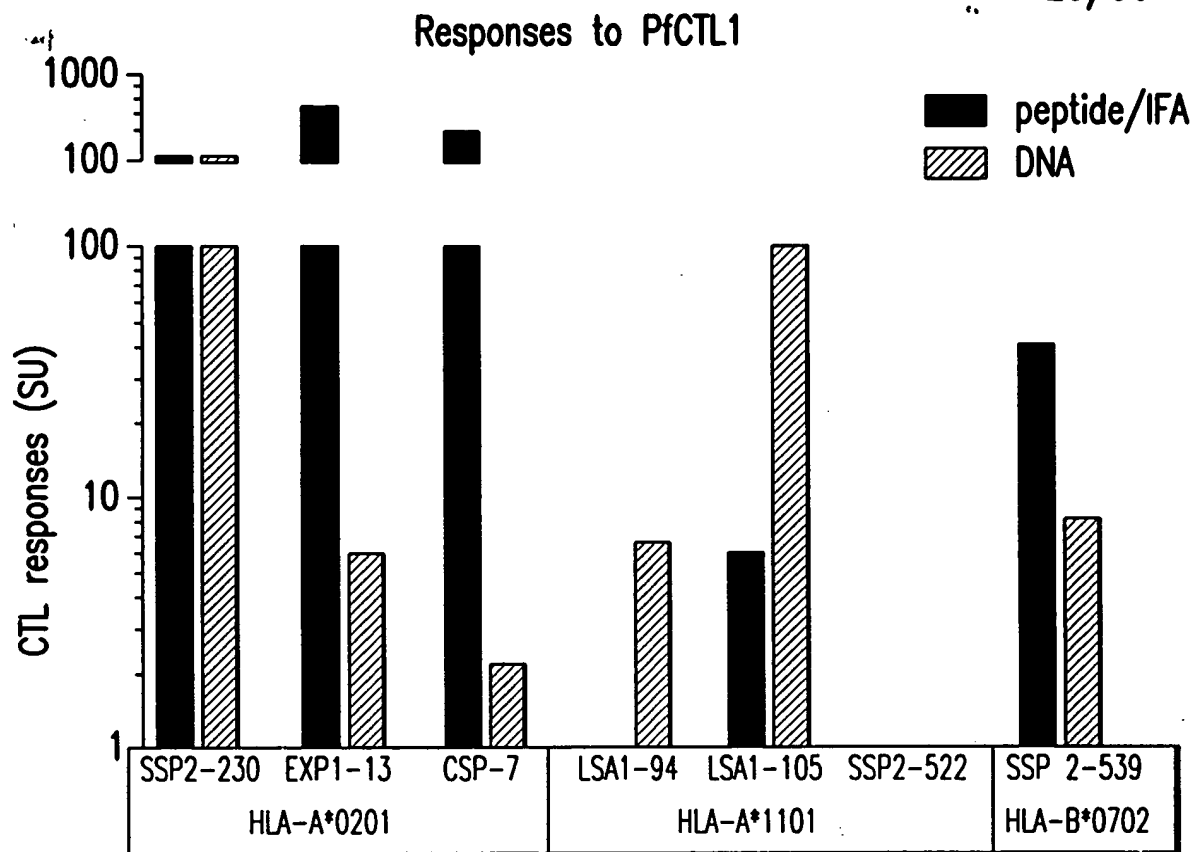
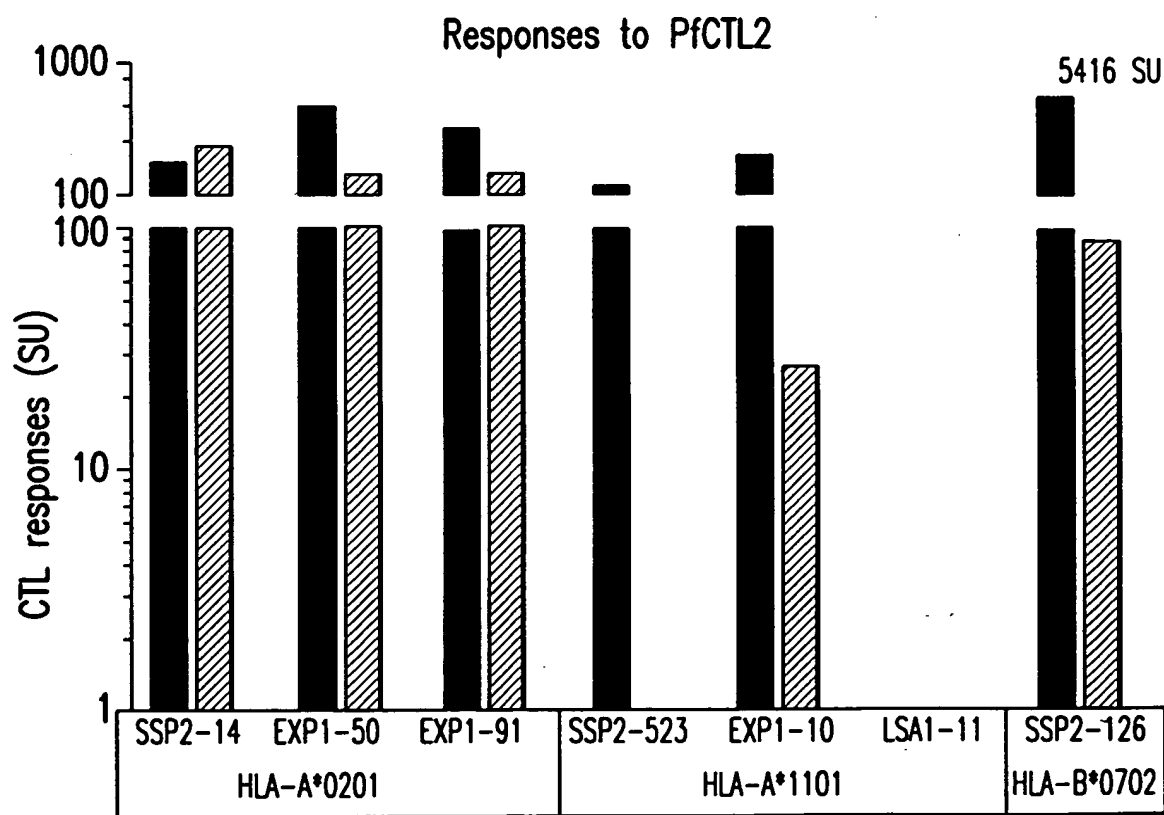


FIG. 14B-1



24/90

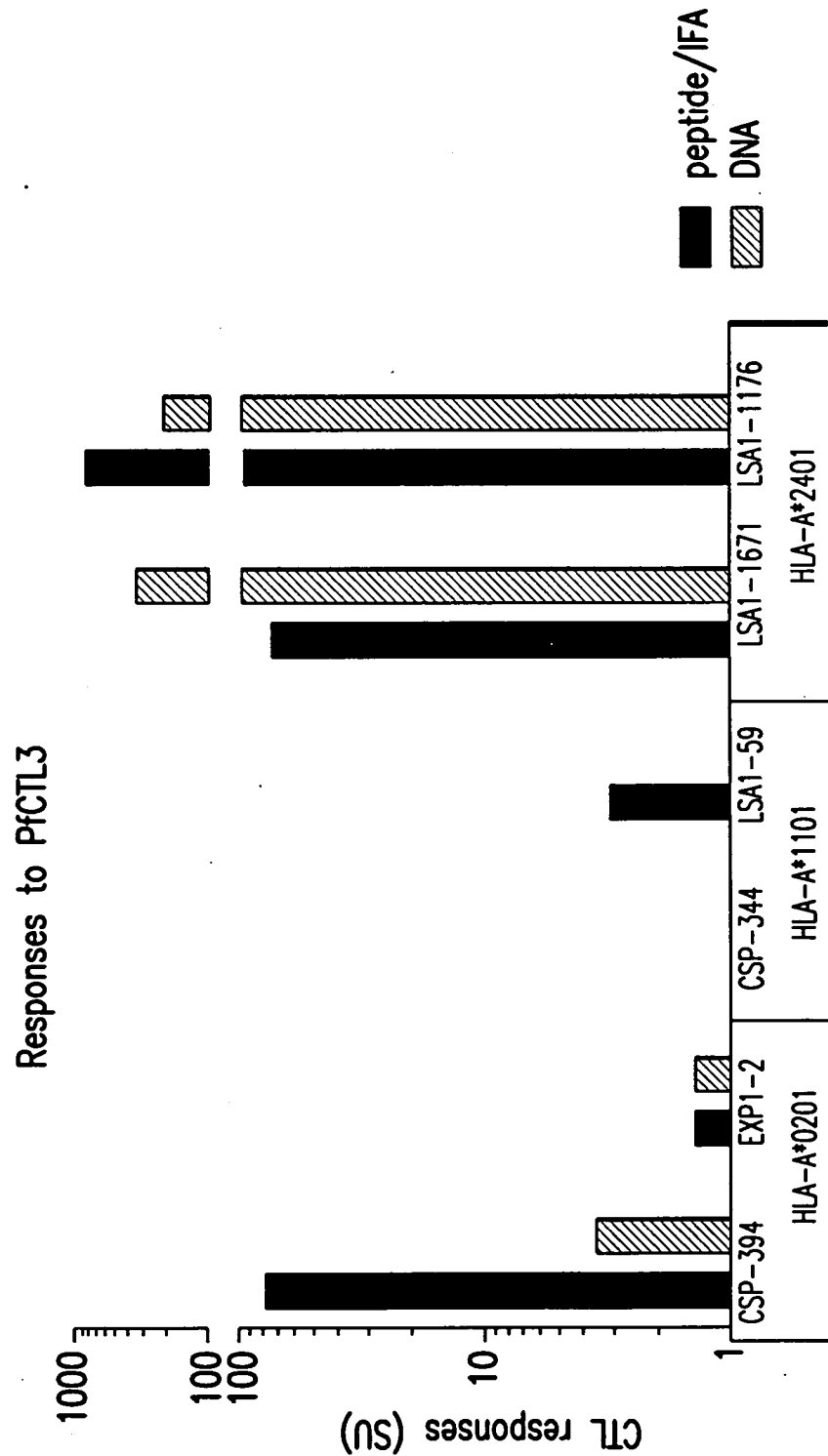


FIG.14B-3

25/90

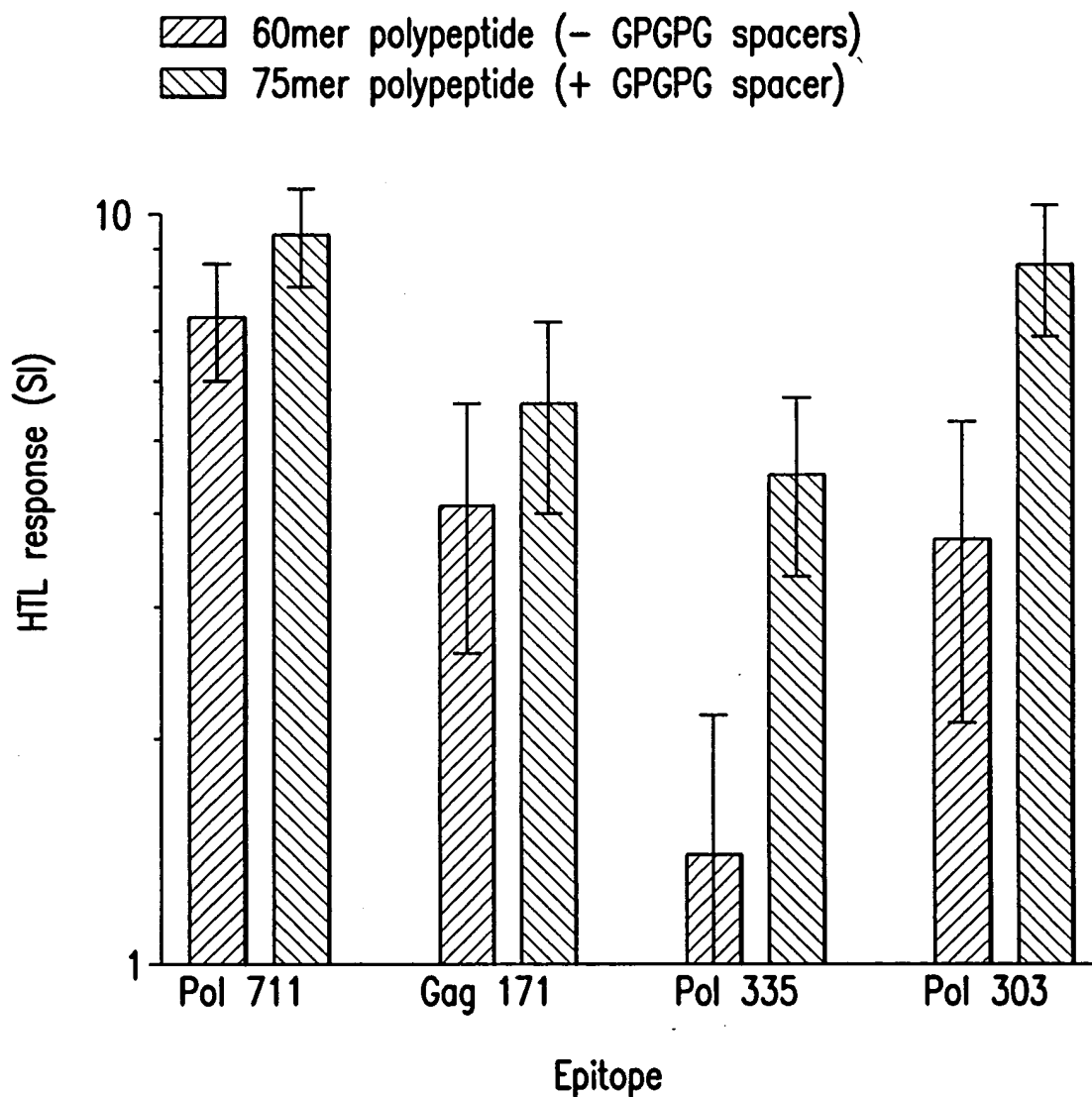


FIG. 15

26/90

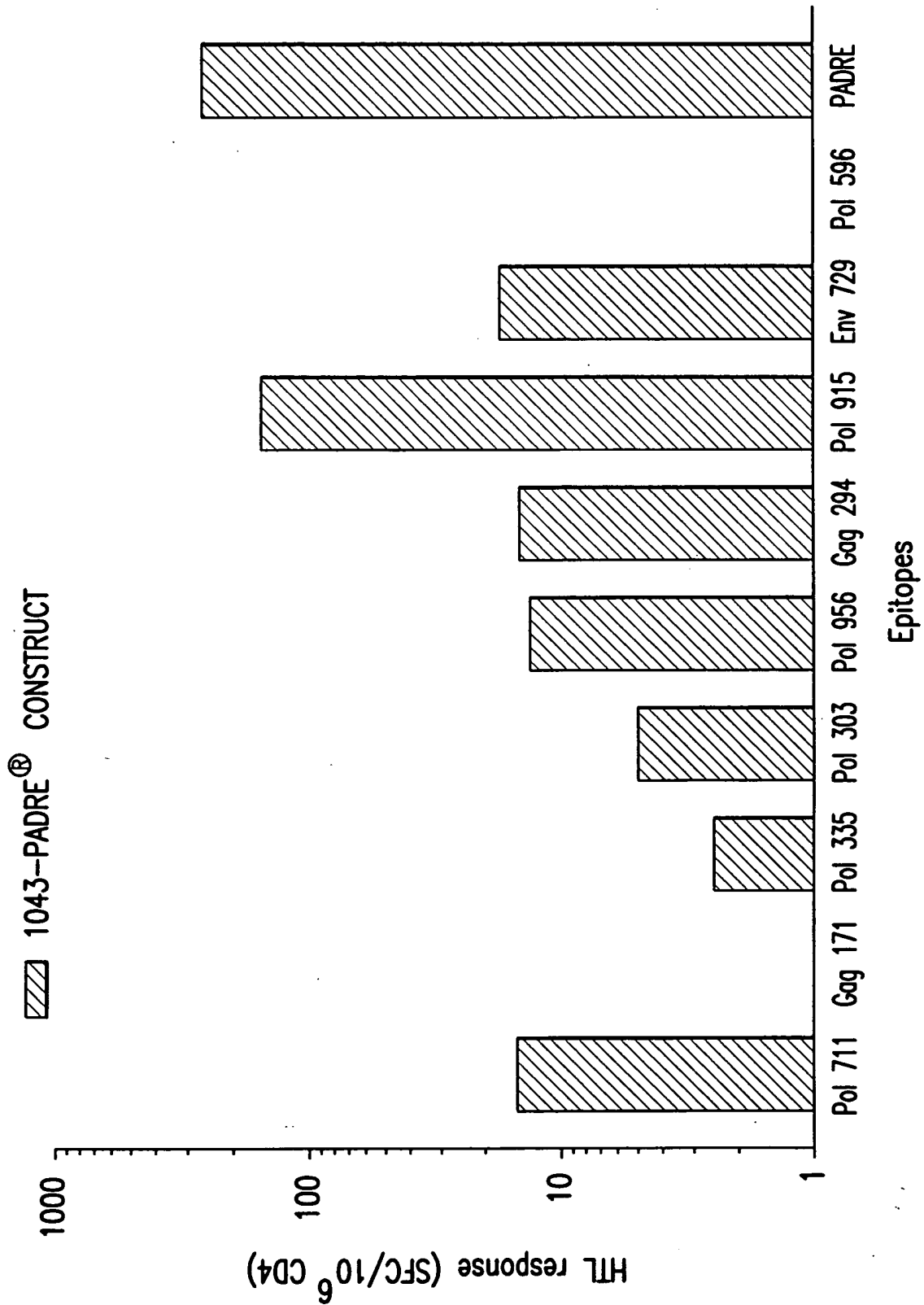


FIG.16

28/90

EP-HIV-1090

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPHIHYCAPAKAKFVAAW
TLKAAAKAFPVRPQVPLGAAKLTPCLVTLGAAVLAEAMSQVKVYLAWVPAHKGAAAAIFQSSMTKKTLFCA
SDAKNIPYNPQSQGVVHKPVHAGPIANVTVYYGVVWKKAAQMAVFIHNFKNAAAYPLASLRSLFNLTFGWC
FKLNRILQQLLFINAKIQNFRVYYRKA AVTIKIGGQLKKVPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCTGTGGGTGCCCGGATCCAGAGGAAAGCTGG
TGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGGGGTGAATGCCGCTTGCCCTAA
AGTCAGCTTCGAACCAATTAAGATCCCCATTACTGTGCACCTGCCAAAGCTAAGTTTGTGGCCGCTTGG
ACCCTCAAGGCCGCTGCAAAAGCCTTCCCAGTGAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCAC
TGTGCGTCACTCTGGGAGCCGCTGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGT
GCCCCGCCACAAGGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACCTCTGTTCTGTGCC
TCCGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGCCGGACCTA
TTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACAGATGGCCGTGTTTATTCA
CAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATCCCTCTTCAACCTGACATTCGGCTGGTGC
TTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTTATCAATGCTAAATCCAGAACTTCCGCGTCTACTATA
GGAAGGCTGCAGTGACTATCAAAATTGGCGGACAACGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGC
AATGACCAACAATCCCCCTATCCCAGTCTGA

HIV-CPT

MGMQVQIQSLFLLLLWVPGSRGIPHIHYCAPAKAAKIQNFRVYYRKA AVTIKIGGQLKKAKFVAAWTLKAAAKV
PLQLPPLKAIFQSSMTKKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYNPQSQGVVKAILKEPVH
GVGAAALTFGWCFKLNVLAEAMSQVNRILQQLLFINAAACPKVSFEPIKVTVYYGVVWKKAAHPVHAGPIA
NAAAYPLASLRSLFNAAATTLFCASDAKNKLVGKLNWANAAAFVVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCTGTGGGTGCCCGGATCCAGAGGAATCCCCA
TTCCTACTGCGCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTATTACAGAAAGGCTGCAGTCAC
CATTAAATCGGCGGACAACCTGAAGAAAGCCAAGTTTGTGGCCGCTTGGACACTCAAGGCCGCTGCAAGGTC
CCTGTCAGCTCCCCCTCTGAAGGCCATCTTCCAGAGCTCCATGACTAAGAACTGACCCCACTGTGTGTGA
CACTCGGGGCCAGATGGCTGTGTTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGC
ACACAAGAACGCCATTCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCAC
GGGGTGGGCGCCGCTGCACTCACTTTTCGGATGGTGCTTTAACTGAACGCCGTGCTGGCTGAAGCCATGAGCC
AGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCCTAAGGTGTCCTTCGAGCCAAT
CAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGCTCATCCTGTCCACGCAGGCCCAATCGCC
AACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAGCCTGTTTAAAGCCGCTGCAACAACCCTCTTTTTCGCGCT
CCGACGCTAAGAATAAACTGGTGGGAAAGCTGAAGTGGGCCAACGCAGCTGCATTCCCTGTGAGGCCACAGGT
CCCCCTCAATATGACTAACAAATCCCCCTATCCCAGTGTGA

FIG.18A

HIV-FT

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLFIMAVFIH
NFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSFEPKIQNFRVYYR
LTFGWCFKLQVPLRPMTYKMTNPPPIPTVYYGVVWVLAEMSQVPIHYCAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGAGGAAAGCTGGTGGGGA
AGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCGTGGCCATCTTCCAGAGCAGCATGACCAAGGT
GACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCAGCTGCTGTTCATCATGGCCGTGTTCATCCAC
AACTTCAAGATCCCCTACAACCCCCAGAGCCAGGGGGTGGTGACCACCTGTTCTGCGCCAGCGATGCCAAGA
TCCTGAAGGAGCCCGTGACGCGGGTGCAGATGGCCGTGTTCATCCACAACCTTCAAGGGCGCCGCCGTGTTCAT
CCACAACCTTCAAGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACCTTCAAGGGTGTACTACAGG
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCCTGAGGCCCATGACCTACAAGATGACCAACAACCCCC
CCATCCCCGTGACCGTGTACTACGGGGTGGCCGTGTGGAAGGTGCTGGCCGAGGCCATGAGCCAGGTGATCCC
CATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTGACCCTG

FIG.18B

30/90

HIV-TC

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAI FQSSMTKKVYLAWVPAHKNAACPKVSFEPIKHPVHAGP
IANLTFGWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLFINTTLFCASDAKNQMVHQAI SPRGAKLV
GKLNWAGAAAIYETYGDTWKAQVPLRPMYKGA AVTVLDVGDAYNAAARYLKDQQLNLTNFPISPINMTN
NPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQGVVKALLQLTVWGIGAAILKEPVHGVNAAAFPI
SPIETVKVWKEATTTLFKAAAVTIKIGGQLKKIYQEPFKNLKAAAVLAEAMSQVNLVGPTPVNIGAAAENVIV
TDSQYKAAAPIHYCAPAKAVIYQYMDDLKAAQA MAVIHNFKNAATYQIYQEPFKPYNEWTLELKAKIQNF
RVYYRKAFVPVRPQVPLGAAAIWGC SGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVT
LNAAMASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASLRSL
F

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCTAGAGGATACTGGC
AAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAGAAGGTATACCTGGCATGGGT
CCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCTTTGAACCCATTAAACACCCAGTGCACGCAGGGCCA
ATAGCGAATTTGACATTCGGGTGGTGCTTCAAAC TAAACAAAATGATCGGCGGCATTGGAGGCTTTATCAAGT
TTAGAGATTACGTGGACCGATTCTATAAAGCCGCTGCCGTATACTCCAGCAGCTACTATTCAACACCAC
TCTCTTCTGCGCTTCAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTA
GGGAAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGCCCAGGTTT
CGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGGAGACGCTTACAACGCTGC
CGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTTCCAATTAGCCCGATAAACATGACAAAT
AACCCACCAATTCCCGTCAATGCTCCCTACAACACTCCAGTATTGCAATCAAAGCCGCTGCTGTCCCCCTGC
AGTCCCTCCTCTGAAAGCTGCGATACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCT
AACAGTTTGGGGAATTGGTGCTGCAATTCTAAAAGAGCCAGTTTCATGGGGTTAACGCCGCCGCTTCCAATC
AGTCCTATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTAAAGGCAGCCGCAGTTACAATTA
AAATAGGGGGCCAACTTAAGAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCCGCTGCAGTGCTCGCCGA
GGCTATGTCACAGGTGAATTTGGTGGACCAACACCCGTAAACATCGGAGCCGCAGCCGAAGTGAACATAGTC
ACCGACTCACAGTACAAAGCCGCTGCAATACCCATACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAAT
ATATGGACGACCTGTATAAGGCCGCCGCGCAGATGGCAGTCTTTATCCACAACTTTAAAAACGCAGCTACTTA
TCAGATCTACCAGGAACCATTCAAACCGTACAATGAGTGGACCTTGGAATAAGGCCAAAATTCAGAACTTC
AGGGTATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGGGATGTT
CTGGAAAAC TGATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAGGCAGCCTGTTGGTGGGC
AGGTATAAAAGCAAAGTTCTGTGGCAGCATGGACGCTTAAAGCAGCCGCAAACTCACTCTCTGCGTGACA
CTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCCCCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAG
TCAACGTAACAGTATATTATGGCGTGCCAGTCTGGAAAAAGCCGCCGCGGCCATAATTTCGGATACTGCAGCA
GCTGAAAAGAGCTATGGCGAGTGACTTCAACCTGAATGCGGCCGCCTACCCCTTGGCATCGTTAAGGTCACTA
TTTTGA

FIG. 18C

HCV. 1

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYL VAYQATVILAGYGAGVRLIVFPDLGVHMWNFISGI
YLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLLADAFLLADARVWMNRLIAFACTCGSSDLYLSAFSLHSYGVAGA
LVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMWNFIPFYGKAIRMYVGGVEHRQLFTFSPRRRLGVRATRKV
GIYLLPNRAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTG
CTGTTCAACATCCTGGGGGGTGGGTGGATCTGATGGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACC
GTGATCCTGGCCGGGTACGGGGCCGGGGTGAGGCTGATCGTGTCCCCGATCTGGGGGTGCACATGTGGAACCTTCATC
AGCGGGATCTACCTGCTGCCCAGGAGAGGACCTAGACTGTACCTGGTGA TAGACACGCTGATGTGGTGCTGGTGGGA
GGAGTGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCTGCTGCTGGCTGATGCTAGAGTGTTGGATGAAC
AGACTGATCGCTTTCGCTTGACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGGAGTG
GCTGGAGCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGA
CTGATCTTTTGTACAGCAAGAAGAAGTTTGGGCTAAGCACATGTGGAATTTATCCCTTTCTATGGAAAGGCTATC
AGAATGTATGTGGGAGGAGTGGAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACA
AGAAAGGTGGGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG*

HCV. 2

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLFTFSPRRYL VTRHA
DVYLLPRRGPRLCTCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAAAILAGYGAGVYL VAYQATVGVAGALVA
FKIPFYGKAIRMYVGGVEHRVLVGGVLA AFLLLADARVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRK
RLIVFPDLGVWMNRLIAFALSASFSLHSYLLFNILGGWVVGIIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCTTGGACACTGAAGGCTGCTGCTCTGCTGTTT
CTGCTGCTGGCTGATGCTCTGATCTTCTGTACAGCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTG
GTGACAAGACACGCTGATGTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTAT
CACATGTGGAACCTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTATCCTGGCTGGATATGGAGCTGGA
GTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTGGCTTTCAAGATCCCATTCTATGGAAG
GCTATCAGAATGTATGTGGGAGGAGTGGAACACAGAGTGCTGGTGGGAGGAGTGCTGGCTGCTTTCTGCTGCTGGCT
GATGCTAGAGTGCTGCCAGGATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCAGCCTAGAAGACTGGGAGTG
AGAGCTACAAGGAAGAGACTGATCGTGTTCAGATCTGGGAGTGTTGGATGAATAGACTGATCGCTTTCGCTCTGAGC
GCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGGAATCTATCTGCTGCCAAACAGA
TGAAAGCTT

HCV. 3s1

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL VTRHADVLGFGAYM
SKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCTGGGCAGCCTGGACACTGAAAGCTGCAGCTCTGCTCTTC
CTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGG
TTTGGCGCTACATGAGCAAGTGACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTATTTCTGGAATCTTT
TGGGCCAAGCACATGTGGAATTTCTGAAAGCTT

32/90

HCV.3s2

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAKFVAAWTLKAAFLLLADARVLSAFSLHSYILAGYGAGVWM
NRLIAFAIPFYGKAIVAGALVAFKVGIIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCTGCTTGGACACTGAAGGCAGCCGC
TTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGC
GCAGGCGTGTGGATGAATCGGCTGATCGCCTTTGCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCC
TGGTGGCATTCAAGGTCGGGATCTACCTCCTGCCTAACCGCTGAAAGCTT

HCV.3s2(-3)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAKFVAAWTLKAAFLLLADARVLSAFSLHSYILAGYGAGVWM
NRLIAFA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCTGCTTGGACACTGAAGGCAGCCGC
TTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGC
GCAGGCGTGTGGATGAATCGGCTGATCGCCTTTGCCTGAGGATCC

HCV.3s3

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWVRMYVGGVEHR
RLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCTTGGACCCTGAAGGCCGCTGC
CAGACTGGGAGTGCGCGCTACACGGAACTCCTGTTTAACATCCTGGGAGGGTGGGTGCGGATGTACGTCGGA
GGCGTCGAGCACAGAAGGCTCATTGTCTTTCCAGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCA
AACTGCCAGGGTGCAGCTTCAGCATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTC
TCCTCGGAGGTATCTGCTGCCAGACGCGGACCCAGGCTGTGAAAGCTT

HCV.PC3

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPDLGVKFWAKH
MWNFIGVAGALVAFKKQLFTFSPRR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGC
TGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAA
TTTTGGGCAAAGCACATGTGGAATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCA
CCTTCTCCCCAAGACGGTGAGGTACC

HCV.PC4

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPL
VKYLLPRRGPRNLNTLCGFADLMGYRMYVGGVEHR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGAT
CCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGC
CGCTAAACAAGCGAGCGCTCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCATG
GGGTACATTCCACTGGTGAAGTATCTGCTCCCAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTG
ATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGATGAGGTACC

HCV.2431(1P)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFAGAAAR
LGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRNLNTLCGFADLMGYRMYVGGVEH
RKLLFNI LGGWVKAALADGGCSGGAYRLIVFPDLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLV
AYQATVAAALLFLLADALIFCHSKKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFK
AAAAKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGCT
CCAGAGGAGTCCTGGTGGGCGGCGTCTGGCAGCCGCTTTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGC
CTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTTGCC
GGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAACAAGCGAGCGCTCCAGC
CCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCT
GCTCCCAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTC
GGCGGAGTCGAACACAGAAAAGTCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACG
GGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACAT
GTGGAATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAAGACGG
AACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCA
TCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAG
CAAGTGACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCAC
ATGTGGAATTTTAAGGCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGGATCC

FIG.18F

34/90

HCV. 4312(1P)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRNLNLC
GFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWNFIGVAGALVAFKKQLF
TFSPRRNGYLVAYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKH
MWNFKKAAAVLVGGVLAFAFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGCTCCAGAG
GAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCAGCCCAGGAACCTGCCTGG
ATGCTCTTTACGATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGC
CTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTGAACACAGAAAAGTCTCT
TCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGT
CTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTTCATCGGGGTGGCCGGAGCCCTGGTCTGCTTTT
AAAAAGCAGCTCTTCACCTTCTCCCAAGACGGAACGGATACCTCGTCGCCCTACCAGGCCACTGTGGCTGCAGCTCTGC
TCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCT
GGGGTTTGGCGCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTTATTTCTGGAATC
TTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAGTCTGGTGGGCGGCGTCTGGCAGCCGCTTTCCTGC
TCCTGGCAGACGCCAGGGTGCTGTCTGCCCTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGAT
GAATCGGCTGATCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGGATCC

AOSI.K

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVKFLLSLGIHLYMDDVVLGVGLSR
YVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTCTT
TCCTAGCGTGAAGTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGTGGGAGTGGGACTGTCCAGG
TACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA

HBV. 1

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVFLSLGIHLYMDDVVLGVGLSR
VARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWSLLVPFVPIIPSSWAFTPARVTGGVFKVGNFTGLYLPDFFPS
VTLWKAGILYKNVSIPTWHLKLVVDFSQFSRSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTCTT
TCCTAGCGTGTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGTGGGAGTGGGACTGTCCAGGTAC
GTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAGCTCCTGGGCTTTTAC
CCCAGCCAGGGTGACCGGAGGAGTGTAAAGGTGGGAAACTTCACCGGCTGTATCTGCCAGCGATTTCTTTCTAGC
GTGACCCTGTGGAAGGCCGGGATCCTGTACAAGATGTGTCCATCCCTTGACCCACAAGCTGGTGGTGGACTTTTCCC
AGTTCAGCAGATCCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

35/90

HBV.2

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVLGVGLSR
YVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSWAFKTPARVTGGVFKVGNFTGLYN
LPDFFPSVKTLWKAGILYKNVSIPTWTHKGAALVDFSQFSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGTCCAGAGGACACACCCTGTGGA
AGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTCTT
TCCTAGCGTGAACCTTCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGTGCTGGGAGTGGGACTGTCCAGG
TACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGTGAATATCCCTATCCC
TAGCTCCTGGGCTTTCAAGACCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAACTTCACCGGCCTGTATAAC
CTGCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGA
CCCACAAGGGAGCCGCTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAGC
TCTGATGCCACTGTATGCCTGTATCTGA

PfCTL.1

MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAYKKAAAAKFVAAWT
LKAAAKAFMKAVCDEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLATSVLKAGVSENI FLKNAAYF ILVNLLIK
AGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAATCCTGAGCGTGT
CCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGCCTCCTGAGGAACCTCCCCTCCGAGAACGAAAG
AGGCTACAAAGCCGCTGCACTGCTCGCCTGCGCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCT
TGGACACTGAAGGCCGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTTG
TGGAGGCCCTCTTTAAGCTACTCCTTACGCAGGGGAACAGCCCCCTTCAAGGCCGCTGCAAAATATAAGCTGGCAAC
CAGCGTGCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAACGCCGCTGCATACTTCATCCTGGTGAATCTGCTC
ATTAAGGCCGGACTCCTGGGGGTGGTCTCTACAGTGTGA

PfCTL.2

MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYF ILVNLLKAALFFI IFNKNAAAK
FVAAWTLKAAKF ILVNLLIFHNFQDEENIGIYKLPYGRN LKAAVLLGGVGLVNFLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGATTCGTGGAGGCC
TGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTCCTGATCAATGCTCTGGCATGCGCCGGCTCGC
TTACAAAAAGTTTTACTTCATTCTGGTCAACCTGCTCAAGGCCGCTCTGTTCTTTATCATTTTTCAATAAAAACGCCGCA
GCTAAGTTTGTGGCCGATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTCACAACTTCC
AAGACGAGGAAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGCAGTCTGCTCGGCGG
AGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCTGGTGAAGGCCGCTCTGGCCGGCTGCTCGGAGTC
GTGTGA

FIG.18H

36/91

PfCTL.3

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGDNEIKAHVLSHNSY
EKNYYGKQENWYSLKKILSVFFLANAAAFIKSLFHFKAALYISFYFIKAKFVAAWTLKAAAKAAAYYIPHQSSLKA
AAGLIMVLSFL

ATGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAGTGTTCTGATCT
TCTTTGACCTGTTCTGAACGCCGCTGCACCCAGCGATGGCAAGTGCAATCTCTACAAGGCCGCTGCAGTGACCTGTGG
AAACGGGATTAGGTGAGGAACTCTTTCACATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCCAAT
TCTTATGAAAAAACTACTATGGAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTGCCA
ACGCCGCTGCAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCAGCTTCTATTTTATTAA
AGCAAATTTGTGGCCGCTTGACACTGAAGGCCGCTGCAAAAGCCGCTGCATACTATATCCCTCACCAGAGCTCCCTG
AAGGCCGCTGCAGGGCTGATCATGGTGCTCTCTTTCTGTGA

PfCTL/HTL(N)

MQVQIQSLFLLLLWVPGSRGSSVFNVNSSIIGLIMVLSFLGPGPGLYISFYFILVNLLIFHINGKIIKNSEGPGPDPDS
IQDSLKESRKLSGPGPGVLAGLLGVVSTVLLGGVGLVLGPGPGLPSENERGYYPHQSSLGPGPGQTNFKSLLRNLGVS
ENIFLKGPDPGFQDEENIGIYGPDPGKYLIVFLIFFDLFLVGPDPGKFIKSLFHFIDGDNEIGPDPGKSKYKLATSVL
AGLLGPGPGLPYGKTNLGPDPGRHNWVNHAVPLAMKLIGPDPGMRKLILSVSSFLFVEALFQEYGPDPGVTCGNGIQV
RGPDPGMNYYGKQENWYSLKKGPDPGPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPDPGKILSVFFLALFFIIFN
KGPDPGHVLSHNSYEKGPDPGKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGTAGTGTTCA
ATGTTGTGAATCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTCACCTGTAAATATTCCACATTAACGGCAAAATAAT
AAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATTCTCTAAAAGAATCGAGGAAGCTCTCCGGACCA
GGCCTGGTGTACTCGCCGGGTGCTGGGAGTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTG
GACCAGGTCTGCCGTCCGAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCAGGCCCCGGACAAAC
CAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACCCGGTCCCGGCTTTAGGAC
GAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAATAACCTAGTGATCGTATTCTTAATTTTTTTTGACCTATTTT
TGGTGGGCCAGGTCCCGAAAGTTCATTAAATCACTCTTCACATTTTTGACGGAGATAACGAGATAGGACCCGGTCC
CGGAAATCAAAGTACAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCAGGGCTCCCTATGGAAAG
ACAAATCTTGGCCCCGGTCCAGGACGGCACAACCTGGGTGAATCATGCGGTTCCATTGGCCATGAACTAATCGGGCCCG
GTCCAGGCATGCGAAACTTGCAATTCTAAGCGTAAGTTCATTTCTGTTCTAGAGGCACTGTTTCAAGAATATGGCCC
AGGACCTGGCGTCACATGTGGAATGGGATCCAGGTGAGAGGACCGGGACCTGGTATGAACTATTACGGTAAACAGGAA
AATTGGTACTCCCTGAAAAAGGTCCAGGCCCCGGCCCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCAGCATGGG
AGAACGTAAAAATGTAATAGGCCATTTCATGAAGGCAGTTTGTGTGCAAGTCGGACCAGGCCAGGAAAAATACTTTCT
TGTCTTCTCTAGCTCTCTTCTTCATCATCTTCAACAAGGGACCAGGGCCAGGTACGTGTTATCCATAACTCTTAT
GAAAAAGGGCCAGGACCTGGGAAATACAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCTGCGCAGGCT
TGGCTTACAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATCTGC

FIG. 181

37/90

Pf33

MGMQVQIQSLFLLLLWPGSRGFMKAVCVEVNVTCGNGIQVRKGLIMVLSFLNAALFHIFDGDNEIKAALLACAGLAYK
KSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLRLNPSENERGYKAAGVSENIFLKNAAYFILVNLLIKAAAILSVSS
FLFVNTPYAGEPAPFKAAKYKLATSVLKAIVFLIFFDLFLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVNLAC
AGLAYKKAKFIKSLFHIFKAAFYFILVNLLKAFLIFFDLFLVKALFFIIFKNYYGKQENWYSLKFVEALFQEYNAAAK
FVAAWTLKAAKILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRNLKA
AHVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGATTTA
TGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAATTCAGGTGAGAAAGGGACTCATCATGGTACTCAG
CTTTCTGAACGCAGCCCTGTTCCACATCTTTGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGACTA
GCCTATAAAAAGAGTTTCTTTTCTGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATAAAG
CAGCTCAGACTAATTTCAAAGCCTGTGAAGAAATCTGCCCTCAGAGAATGAAAGGGGTACAAAGCCGCCGGCGTGTCTC
CGAGAATATTTTCTGAAGAACGCCGCTGCTTATTTTATACTCGTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCA
GTGTCCAGCTTTCTGTTTGTAAACACACCATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTG
CCACATCAGTATTGAAAGCAGCTGTGTTTTGATATCTTTGATCTTTTTTAACTACTACATACCTCATCAGTCTAG
TCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGTCTTACTTGAGGAGTTGGCCTCGTGTTGAAC
CTCGCGTGCGCAGGTCTGGCCTACAAAAAGCGAAATTCATCAAGTCTCTGTTCCACATTTTTAAAGCCGCATTCTATT
TCATACTAGTGAACCTTCTCAAAGCTTTCCTGATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTT
TAACAAAAATTATTACGGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAGATCCTATCGGTCTTCTTTCTCGCTAATGCCGTAT
TAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAGGCATCTACAAAGCCGCAGCACTGTACATTTT
ATTCTACTTCATCAAGGCCTTCATACTGGTCAACCTTCTGATATTTTATAATGCAGCACTGCCATATGGGAGAACCAAC
TTGAAAGCGGCCACGTGTTGAGCCACAACCTCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCTCTGA
TTTGA

TB.1

MQVQIQSLFLLLLWPGSRGRMSRVTTFTVKALVLLMLPVVNLMIPTAAAVVKALVLLMLPVGAGLMTAVYLVGAAAMA
LLRLPVKRMFAANLGVNSLYFGGICVGRLLPLVPAVNAAAARLMIGTAAAGFVVALIPLVNAM
TYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGGATGAGCAGAGTGACCA
CATTCAGTGTCAAGGCCCTGGTGTCTGATGCTCCCGTCTGTGAACCTGATGATCGGCACCGCTGCAGCCGTCTGTAA
AGCTCTCGTCTGCTCATGCTCCCTGTGGGAGCAGGGCTGATGACAGCCGTGTACCTGGTCCGGCTGCAGCCATGGCC
CTCCTGCGGCTGCCAGTGAAGCGCATGTTTGTGCAAATCTGGGAGTCAACTCCCTCTATTTGGGGGCATTTGCGTGG
GAAGGCTGCCCCCTGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTGCGCGCTTGGAATCTGAAGGCAGCCGC
TAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTTCTGGTGCCTGATTCCCTGGTGAACGCCATG
ACATACGCAGCTCCTCTGTTTGTGGGAGCCGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

FIG.18J

38/90

BCL A2 #90

MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYLSGANLNVG
AAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAAATVGIMIGVNAKLCPVQL
WV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAATTATGATCGGCC
ATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAAGGTGGCCGAAATTGTGCACTT
TCTCAACGCAAAGGTGTTTGGTTCCCTGGCTTTTGTCAATGCCTATCTGAGCGGCGCTAACCTCAACGTCGGA
GCCGCTACCTCCAGCTGGTCTTCGGCATCGAGGTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCA
AGGCTGCAGCAAAGGCTGCCGCCGTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGAC
TAGGGTCAATGCTGCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAACTGTGCCCAGTGCAACTG
TGGGTGTGA

BCL A2 #88

MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANLNVGAAYLQL
VFGIEVNIMIGHLVGVNRLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATVGIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAGTCGTGCTGGGAG
TCGTCTTCGGCATTAAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTGAAGGCCGAGCTAAAGTGGC
AGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAATCTGAACGTCGGCGCTGCCTATCTGCAGCTC
GTGTTTGAATTGAAGTGAACATCATGATTGGACATCTGGTGGCGTGAACAGGCTGCTCCAGGAACTGAGC
TGGTCAACGCTAAAGTGTTCCGGTCTCTCGCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACTCTGGGTCAA
TGCCGCAGCCGCTACAGTGGGGATCATGATCGGCGTGAACCTCATGCCTCCACCAGGGACCAGAGTGTGA

BCL A2 #63

MQVQIQSLFLLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLQETELVNAKVAEIVHFL
NAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTR
V

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAGCTCTGCCCCG
TGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTGAACATCATGATCGGACACCT
GGTCCGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAATGCCAAGGTGGCTGAAATTGTCCATTTCTG
AATGCCAAAGTGTTCCGGCTCTCTCGCTTTTCGTGAACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCG
CATACCTCCAGCTCGTCTTTGGGATTGAGGTGAATGCCGCAGCTAAATTTGTGCTGCCTGGACCCTGAAGGC
AGCAGCCAAGGCTGCCGCAGTGGTGTGGGAGTGGTGTGGGAATCAATTCCATGCCTCCACCAGGCACTAGA
GTGTGAGGATCC

FIG.18K

39/90

Prostate 1

LTFFWLDRSVKAAAVLVHPQWVLT VKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVKAAIMYSAHD
TTVKAAAF LTPKKLQCVNAMNDQLMFLNAGLPSIPVHPVKAAALGTTTCYVGAAILLWQPIPVNFLRPRSLQC
VKAF LTL SVTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTGACATTTTTTTT
GGCTGGATAGATCGGTTAAGGCTGCAGCCGTGCTTGTTTCATCCCAGTGGGTCTTGACCGTAAAGGCTGCCGC
GCTGCTACAAGAAAGAGGGGTGCGATACATCAAAGCTGCTCTCCTCTTGAGTATTGCGCTAAGTGTAACCCG
CTAGTTTGTAATGGGGTGTTACAAGGTGTGAAAGCGGCGATTATGTACAGTGCACGACACTACCGTAAAAG
CAGCCGCTTTCTGACCCCAAAAAA ACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAA
CGCTGGCTTACCTTCTATACCGGTTTCATCCAGTCAAGGCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCA
GCGATACTTCTTTGGCAGCCCATACAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAGCATTCC
TTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACA ACTTGGGCGCGGCCAC
ACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGACTCTAAAGGCCGCGAGCA

HIV-1043

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGP GPGWFEVNTPLVKLWYQGP GPGYRKILRQRKID
RLIDGPGPGQHLLQLTVWGIKQLQGP GPGGEIYKRWIILGLNKIVRMYGPGPGQGQMVHQAI SPRTLNGP GPG
IKQFINMWQEVGKAMYGPGPGWAGIKQEFGI PYNPQGP GPGKTA VQMAVF IHNFKRGP GPGSPAIFQSSMTKI
LEPGPGPEVNIIVTDSQYALGIIGPGPGHSNWRAMASDFNLPPGP GPGAETFYVDGAANRETKGP GPGGAVVI
QDNSDIKVVP GPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACCTGGGCAGAAAC
AGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAGGTTGGGAGTTTGTGAACACACC
ACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGATACCGTAAAATCCTGAGGCAAAGAAAGATAGAT
CGCCTCATTGATGGCCCCGGGCCAGGCCAGCACCTTCTGCAGCTTACAGTGTGGGGAATTAACAGCTGCAGG
GGCCGGGCCCCGGGGGGGAAATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGG
CCCTGGACCCGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAGGA
ATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTGGATGGGCAGGGA
TAAACAGGAGTTTGAATCCCTTACAATCCCAGGGTCTGGGCCAGGTAACAGGCAGTGCAGATGGCCGT
GTTCAATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGCCAGCTATATTTCAAAGTTCGATGACCAAAATC
TTGGAGCCCGGCCAGGGCCGGGCGAAGTGAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGC
CCGGACCAGGGCATTCCAATTGGCGGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGC
GGAACTTTCTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCATT
CAGGACA ACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCGGGTTCAGAAAGTATACCGCCTTCACTATTC
CGTCCATCAACAATGAGTGA

FIG. 18L

40/90

HIV-1043 PADRE

MEKVYLA WVP A H K G I G G G P G P G Q K Q I T K I Q N F R V Y Y R G P G P G W E F V N T P P L V K L W Y Q G P G P G Y R K I L R Q R K I D
R L I D G P G P G Q H L L Q L T V W G I K Q L Q G P G P G G E I Y K R W I I L G L N K I V R M Y G P G P G Q G Q M V H Q A I S P R T L N G P G P G
I K Q F I N M W Q E V G K A M Y G P G P G W A G I K Q E F G I P Y N P Q G P G P G K T A V Q M A V F I H N F K R G P G P G S P A I F Q S S M T K I
L E P G P G P G E V N I V T D S Q Y A L G I I G P G P G H S N W R A M A S D F N L P P G P G P G A E T F Y V D G A A N R E T K G P G P G G A V V I
Q D N S D I K V V P G P G P G F R K Y T A F T I P S I N N E G P G P G A K F V A A W T L K A A A

A T G G A G A A G G T G T A C C T G G C C T G G G T T C C A G C C C A C A A A G G C A T C G G G G G A G G G C C C G G A C C T G G G C A G A A A C
A G A T C A C C A A G A T C C A G A A C T T C C G G G T A T A C T A C C G G G G A C C T G G T C C A G G T T G G G A G T T T G T G A A C A C A C C
A C C T T A G T A A A G C T C T G G T A C C A G G G C C C G G T C C C G G A T A C C G T A A A A T C C T G A G G C A A A G A A A G A T A G A T
C G C C T C A T T G A T G G C C C G G G C C C A G G C C A G C A C C T T C T G C A G C T T A C A G T G T G G G G A A T T A A C A G C T G C A G G
G G C C G G G C C C G G G G G G A A T T T A T A A A A G G T G G A T C A T T C T G G G T C T G A A C A A G A T C G T C C G C A T G T A T G G
C C C T G G A C C C G G A C A G G G G C A G A T G G T C C A C C A A G C A A T C A G C C C T C G A A C C T T G A A T G G A C C G G G C C C A G G A
A T C A A G C A A T T C A T T A A C A T G T G G C A A G A A G T T G G T A A G G C T A T G T A C G G T C C C G G C C C T G G A T G G G C A G G G A
T A A A C A G G A G T T T G G A A T C C C T T A C A A T C C C C A G G G T C C T G G G C C A G G T A A A C A G G C A G T G C A G A T G G C C G T
G T T C A T T C A T A A T T T T A A G C G G G G C C C T G G A C C T G G C A G C C C A G C T A T A T T T C A A G T T C G A T G A C C A A A A T C
T T G G A G C C C G G C C C A G G G C C G G G C G A A G T G A A C A T T G T C A C A G A T T C T A G T A T G C C C T C G G C A T C A T A G G G C
C C G G A C C A G G G C A T T C C A A T T G G C G C G C C A T G G C G T C T G A C T T T A A T C T A C C T C C T G G G C C A G G C C C T G G C G C
G G A A A C T T T C T A T G T G G A C G G C G C T G C A A A C A G G G A G A C T A A G G G A C C C G G A C C C G G C G G C G C T G T A G T C A T T
C A G G A C A A C T C A G A C A T C A A G G T G G T T C C C G G T C C A G G C C C C G G G T T C A G A A A G T A T A C C G C C T T C A C T A T T C
C G T C C A T C A A C A A T G A G G G C C C C G G C C C A G G T G C C A A G T T C G T G G C T G C C T G G A C C C T G A A G G C T G C C G C T T G
A

HIV 75mer

E K V Y L A W V P A H K G I G G P G P G Q G Q M V H Q A I S P R T L N G P G P G S P A I F Q S S M T K I L E P G P G P G F R K Y T A F T I P S I N
N E

G A G A A G G T G T A C C T G G C C T G G G T G C C T G C C C A C A A G G G A A T C G G A G G A C C T G G C C C T G G A C A G G G A C A G A T G G
T G C A C C A G G C C A T C A G C C C T A G G A C C C T G A A C G G A C C T G G A C C T G G A A G C C C T G C C A T C T T C C A G A G C A G C A T
G A C C A A G A T C C T G G A G C C C G G A C C T G G A C C T G G A T T C A G G A A G T A C A C C G C C T T C A C C A T C C C C A G C A T C A A C
A A C G A G T G A

FIG. 18M

PfHTL

MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKSKYKLATSVL
AGLLGPGPGQTNFKSLRLNLGVSEGPGPSSVFNVVNSSIGLIMGPGPGVKNVIGPFMKAVCVEGPGPGMNY
YGKQENWYSLKKGPGPGLLAYKFVPGAATPYGPGPGPDSIQDSLKESRKLNPGPGLLIFHINGKIIKNSE
GPGPGAGLLGNVSTVLLGGVGPGPVKYKIAGGIAGGLALLGPGPGMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGGCAC
AACTGGGTGAATCATGCTGTGCCCTGGCTATGAAGCTGATCGGCCCTGGACCAGGGAATGCAACCTCTAC
GCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTGGGAAATCCAAGTATAAGCTCGCTACCTCT
GTGCTGGCAGGCCTGCTCGGACCAGGCCCCGGACAGACAAATTTCAAAGCCTGCTCAGAAACCTGGGAGTG
TCCGAGGGGCCTGGCCCAGGATCTAGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCC
GGACCTGGGGTGAAAAATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTGCGAAGGACCCGGGCCTGGCATG
AACTACTATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTACAAG
TTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCAGGACTCTCTCAA
GAGAGCCGGAAGTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACATCAATGGCAAATTATCAAGAAC
AGCGAGGGACCTGGGCCAGGCGCCGACTGCTGGGGAACGTGTCCACCGTCCTGCTCGGCGGAGTGGGGCCC
GGCCCTGGGAAGTACAAGATCGCTGGAGGGATCGCAGGCGGACTGGCCCTCCTGGGCCAGGACCAGGGATG
CGCAAAGTGGCTATTCTCTCTGTCTCCAGCTTTCTGTTTGTGTGA

FIG.18N

42/90

Protein	Sequence	Restriction
HIV gag 386	VLAAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAI SPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDL Y	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGC SGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIG. 19A

43/90

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMV	HLA-DR
HIV pol 596	WEFVNTPLVVKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAI SPRTL N	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEF GIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPR L	HLA-A2
HCV NS1/E2 726	LLFLL LADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSRR	HLA-A3
HCV NS1/E2 632	RMVVGGEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDP SHITA	HLA-A1

44/90

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSCGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCDEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENI FLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

45/90

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTIVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

46/90

Protein	Sequence	Restriction
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIG.19E

47/90

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN ¹
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILT	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
927.15	pol 642	ALMPYACI	95	A2	12.9	4
1083.01	core 141	STLPETTIVRR	95	A3/A11	735/4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4/15.6	5
1069.15	pol 150	TLWKAGILYK	100	A3/A11	2.1/33	2
1069.20	pol 388	LVVDFSQFSR	100	A3/A11	6875/17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174/117	3
1090.11	pol 531	SAICSVRR	95	A3/A11	2189/29	3
1142.05	pol 629	KVGNTGLY	95	A3/A1	58/365	2
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249/8	3
988.05	core 19	LPSDFFPSV	45	B7	3026.8	4
1145.04	env 313	IPISSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1039.06	env 359	WMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETIVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAIFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	EYLVSGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

¹ XRN = Cross binding, number of HLA types in the supertype panel of 5 for which significant binding as detected

FIG.20A

48/90

HBV2 EpiGene													A1 & A24 epitopes															
signal	Pol 149	Core [®] PADRE	Pol 562	Pol 538	Pol 455	Env 183	Core 141	Pol 665	Env 335	Env 313	Pol 354	Pol 629	Core 19	Pol 150	Pol 47	Pol 388	Pol 531	Env 359	Pol 745	Pol 429	Core 419	Env 332	Pol 392	Core 137	Pol 415	Core 117	Pol 642	
	A3		A2	A2	A2	A2	A3	A3	A2	B7	B7	A3	A3	B7	A3	A3	A3	A1	A24	B7	A1	A24	A24	A1	A1	A1	A24	A2

Core 117	Pol 415	Pol 745	Pol 429	core 419	Pol 392	Core 137	Env 359	Env 332	Pol 642
A24	A1	A24	B7	A1	A24	A1	A1	A24	A2

FIG.20B

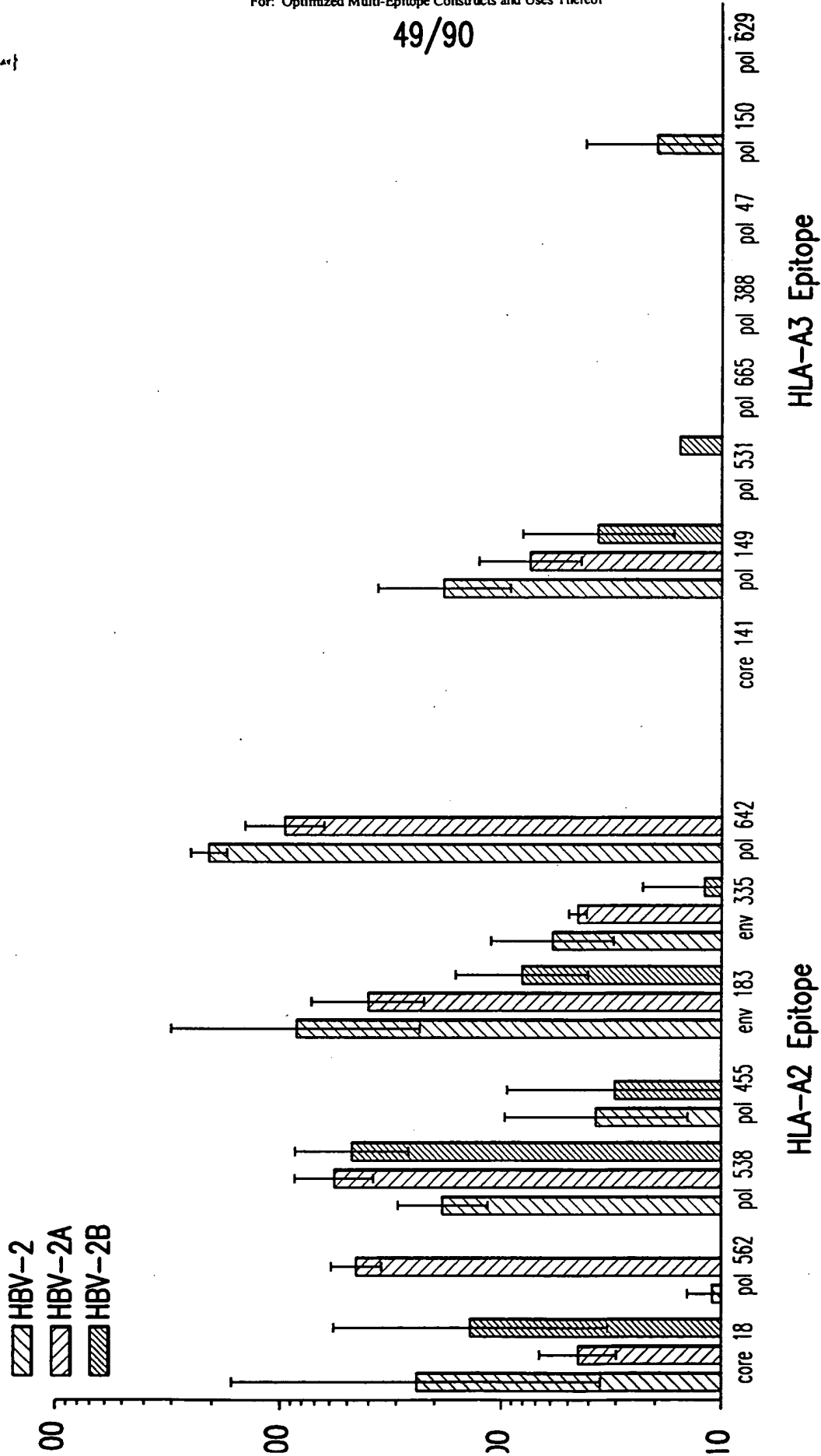


FIG. 20C

50/90

HBV-2

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFFPSVNFLLSLGIHLYMDDVVLGVGLS
RYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAWLSLLVPFVNIPSSWAFKTPARVTGGVFKVGNFTGL
YNLPSDFFPSVKTLWKAGILYKNVSIPTWTHGAALVDFSQFSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCCTGTGG
AAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTT
TTTCCTAGCGTGAACCTTCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGTCTGGGAGTGGGACTGTCC
AGGTACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGG
CAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGTGAATATCCCT
ATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTAAAGGTGGGAAACTTCACCGGCCTG
TATAACCTGCCCAGCGATTTCTTTCTAGCGTGAAGACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATC
CCTTGACCCACAAGGGAGCCGCTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATCCGCTATCTGCTCCGTGGTG
AGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

FIG.20D

HBV-2A

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFFPSVNFLLSLGIHLYMDDVVLGVGLS
RYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAWLSLLVPFVNIPSSWAFKTPARVTGGVFKVGNFTGL
YNLPSDFFPSVKTLWKAGILYKNVSIPTWTHGAALVDFSQFSRNSAICSVVRRKAWMMWYGPSLYKKYTSFPWLLN
AHPAAMPHLLKAAADLLDTASALYNAAARFSWLSLLVPFNAASWPKFAVNLKLTFGRETVLEYKALSLDVSAAFYGA
AEYLVSFGVWGAALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCCCTGTGG
AAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCCTAGCGATTTT
TTTCCTAGCGTGAACCTTCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGTCTGGGAGTGGGACTGTCC
AGGTACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGG
CAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGTGAATATCCCT
ATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTAAAGGTGGGAAACTTCACCGGCCTG
TATAACCTGCCCAGCGATTTCTTTCTAGCGTGAAGACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATC
CCTTGACCCACAAGGGAGCCGCTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATAGCGCCATCTGTTCCGTCTGT
AGAAGGAAAGCCTGGATGATGTGGTACTGGGGTCTAGTCTGTATAAGAAGTACACCTCATTCCCATGGCTCTTGAAT
GCCCATCCCGCTGCAATGCCACACCTGCTTAAAGCTGCGGCGGATCTGCTGGACACAGCCTCAGCTTTATATAATGCT
GCAGCAAGATTCTCCTGGTTGTCTCTTAGTGCCCTTCAACGCAGCTTCTGGCCAAAATTTGCCGTTCCGAACCTG
AAGCTCACTTTTGAAGAGAGACAGTACTTGAATACAAAGCACTAAGCCTTGACGTGTGACGAGCCTTCTACGGAGCA
GCAGAATATCTAGTATCTTTTGGGGTCTGGGGCGCAGCCCTCATGCCTCTATACGCCTGCATTTGA

FIG.20E

HBV - 2B

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAFLPSDFFPSVNFLLSLGIHLYMDDVVL
GVGLSRYVARLFLLTRILTISTLPETTIVRRQAFTFSPTYKGAAWLSLLVPFVNIPISSWAFKTPARVTGG
VFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPTHKGAALVVDQSQFSRNSAICSVVRRKEYLVSGV
WGLSLDVSAAFYNAAKYTSFPWLLNAHPAAMPHLLKAAADLLDTASALYNSWPKFAVPNLKLTFGRETVLEY
KAAWMMWYWGPSLYKAAARFSWLSLLVPFGAAALMPYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCTGAAGGCTGCCGCTTTCCTGCC
TAGCGATTTCTTTCCTAGCGTGAACCTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAG
AGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCT
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGA
GTGTTTAAGGTGGGAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGT
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT
TTCCAGTTTCAAGCAGAAATTCAGCAATTTGTTCCGGTGGTGAGAAGAAAGGAATATCTTGTTTCATTTGGCGTC
TGGGGGCTGTCACTGGATGTAAGTGCGGCATTTTACAATGCCGCCGCAAAATATAAGCTTCCCATGGCTCC
TAAACGCACACCCAGCTGCAATGCCGCATCTACTGAAAGCAGCCGCTGACCTCTTAGACACTGCCTCCGCTCT
GTACAACTCTTGGCCCAAGTTTGCCGTGCCTAATCTCAAGTTGACCTTCGGTAGAGAGACAGTCTTAGAATAC
AAAGCGGCCTGGATGATGTGGTACTGGGGACCCTCTCTGTATAAAGCCGCTGCAAGGTTCTCCTGGCTTAGCC
TTCTCGTACCATTTCGGAGCAGCTGCCCTAATGCCTTTGTACGCATGCATCTGA

FIG.20F

52/90

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFFPVS	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
927.11	pol 562	FLLSLGHL	95	A2	7.8	3
1090.77	pol 538	YMDVVLGV	90	A2/A1	6.4	5
1083.01	core 141	STLPETWRR	95	A3/A11	735/4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4/15.6	5
1090.11	pol 531	SAICSVRR	95	A3/A11	2189/29	3
1090.10	pol 665	QAFTEPTKY	95	A3/A11	249/8	3
1145.04	env 313	TPSPSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPPLL	100	B7	56.6	4
1147.05	pol 530	FPHCLAFSYM	95	B7	58.5	5
1039.06	env 359	WMWYMGPSLY	85	A1	16.3	3
1448.01	core 419	DLDDIASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAIFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	EYLVSGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWILL	85	A24	1.0	3

FIG.21A

	Pol	Core [®]	Pol	Env	Pol	Env	Pol	Core	Pol	Env	Pol	Core	Pol	Env	Pol	Core	Pol	Env	Core	Pol
signal	392	PADRE	429	149	183	415	745	332	354	117	538	419	530	359	531	562	313	335	18	137
	A24	A3	B7	A3	A2	A1	A24	A24	B7	A24	A2	A1	B7	A1	A3	A2	B7	A2	A2	A1
																				A3
																				665

[illegible]

FIG. 21B

54/90

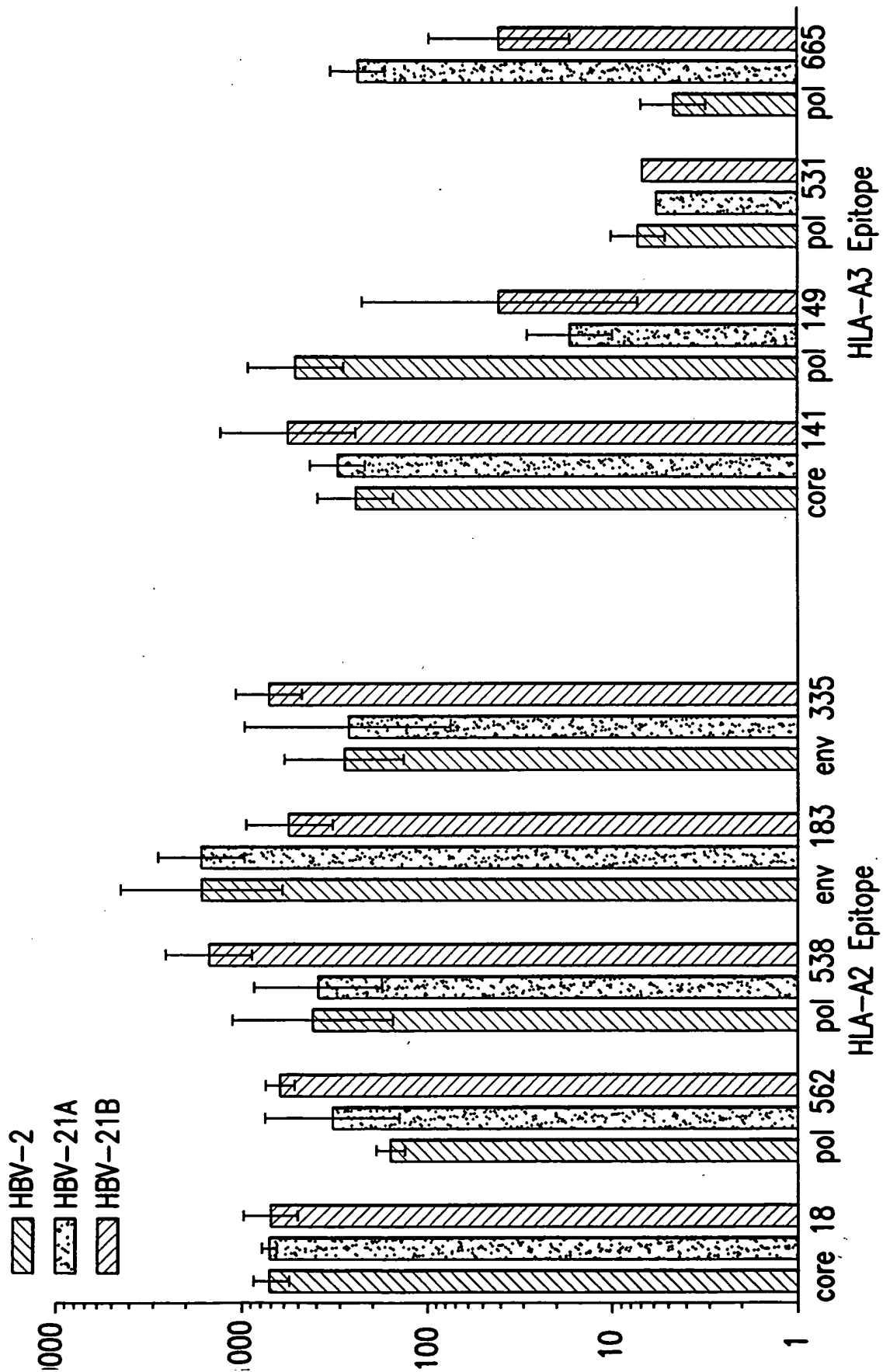


FIG. 21C

HBV - 21A

MGMQVQIQSLFLLLLWVPGSRGWSWPKFAVPNLKAAAAKFVAAWTLKAAAKSTLPETTVVRRKHPAAMPHLLKAAAH
WKAGILYKKAFLLTRILTIGALS LDVSAAFYNAAAKYTSFPWLLNAAARFSWLSLLVPFNAATPARVTGGVFKA
AEYLVSFGVWGAAAYMDDVVLGVNDLLDTASALYNAAAFPHCLAFSYMKA
AAWMMWYWGPSLYKAASAICSVVRKFNLLSLGIHLNIPSSWAFKAAWLSLLVPFVNAFLPSDF
FPSVKLTFGRETVLEYKQAF TFSPTYK

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATCTTGGCCTAAA
TTCGCAGTGCCAAACCTTAAAGCCGCGGCTGCTAAGTTCGTAGCTGCCTGGACACTAAAGGCCGCGCTAAGAGCACA
CTGCCAGAGACCACCGTGGTCCGGCGAAAAGCATCCAGCCGCAATGCCCACTTGCTCAAAGCAGCCGCCCACTCTT
TGGAAGGCTGGGATATTGTACAAGAAAGCCTTCCTTCTGACCAGGATATTA
ACTATCGGAGCTCTGTCACTCGACGTTCTGCTGCCCTTCTACAACGCGGCGGCAAAATACACTAGCTTTCCATGGCTACTCAACGCAGCCGCCAGATTTTCTTGG
CTATCACTACTGGTGCCATTTAATGCAGCAACACCTGCTAGAGTGACTGGCGGCGTCTTTAAAGCAGCCGAGTACTTG
GTGAGCTTTGGCGTCTGGGGTGCAGCGGCATATATGGATGATGAGTGTTAGGGGTGAACGACCTCCTGGACACAGCC
AGTGCCTGTACAATGCAGCTGCATTCCCGCATTGCCTAGCCTTCAGTTATATGAAAGCAGCAGCCTGGATGATGTGG
TACTGGGGACCGTCCCTTTATAAAGCAGCTTCAGCAATCTGTTCCGTTGTGAGGAGAAAAAACTTTTTACTCTCCCTC
GGTATTCACCTGAACATTCCCATCCCTTCCTCATGGGCATTCAAAGCCGCTTGCTGAGTCTACTCGTACCTTTCGTT
AATGCATTTCTGCCAGCGACTTTTTCCCTCGGTAAAACTGACATTCGGACGCGAAACAGTCTTGAATATAAGCAG
GCCTTCACGTTCTCACCAACCTATAAATGA

FIG. 21D

HBV - 21B

MGMQVQIQSLFLLLLWVPGSRGYMDDVVLGVNAAAEYLVSFGVWNDLLDTASALYGA
AHLWKAGILYKKAFLPSDFPSVKAFPHCLAFSYMKAARFSWLSLLVPFNAASWPKFAVPNLKAAAQAF
TFSPTYKNAAASAICSVVRKAFLLTRILTINIPSSWAFKAAWMMWYWGPSLYKAAATPARVTGGVFKA
ANFLLSLGIHLNLTFGRETVLEYKHPAAMPHLLKAASTLPETTVVRRKWSLLVPFVNAAAAKFVA
AWTLKAAAKSLDVSAAFYNAAAKYTSFPWLL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATACATGGATGAC
GTTGTGTTAGGCGTTAATGCAGCCGCAGAATATCTCGTGTCATTCCGGCGTCTGGAACGACCTGTTGGACACTGCATCT
GCTCTGTACGGTGCAGCCCATAACCTGTGGAAGGCCGGAATCCTCTACAAAAAGGCATTCTACCTAGCGACTTTTTT
CCTTCAGTGAAAGCCTTCCCACATTGCCTAGCATTCTCGTATATGAAAGCGGCTAGGTTCTCATGGCTTAGTCTTCTA
GTACCTTTCAATGCCGCCTCCTGGCCCAAATTCGCCGTACCAAATCTAAAAGCGGCCGCGCAGGCCTTTACATTCTCT
CCGACTTATAAAAAATGCAGCAGCCTCCGCTATTTGTAGCGTCGTGCGCCGAAAGGCCCTCCTGCTAACCCGGATTTTG
ACGATAAACATCCCCATCCCTTCTAGCTGGGCTTTCAAAGCAGCATGGATGATGTGGTACTGGGGTCCCAGCTTATAC
AAAGCTGCGGCAACCCAGCAAGAGTGACAGGGGCGTGTTAAGGCCGCAACTTCCTCCTGAGTCTCGGAATACAC
CTGAACCTTAACCTTTGGGAGAGAGACAGTACTGGAGTATAAACACCCAGCAGCTATGCCGCACCTACTCAAAGCCGCT
TCAACACTCCCAGAAACAACTGTAGTGAGGAGAAAAATGGCTCTCCCTGCTTGTCCCATTGTCAACGCCGCCGCGCT
AAGTTTGTGGCCGCTTGACACTTAAGGCTGCAGCAAAGTTGTCACTTGATGTTAGTGCAGCGTTCTATAACGCAGCT
GCAAAATACACTTCCTTTCCCTGGCTGCTGTGA

56/90

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILT I	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
1083.01	core 141	STLPETT VRR	95	A3/A11	735/4.5	4
1147.16	pol 149	HTLWKAG ILYK	100	A3/A1	15.4/15.6	5
1069.20	pol 388	LVVDFSQFSR	100	A3/A11	6875/17	3
1069.16	pol 47	NVSI PWTHK	100	A3/A11	174/117	3
1090.11	pol 531	SAICSVRR	95	A3/A11	2189/29	3
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249/8	3
988.05	core 19	LPSDFFPSV	45	B7	3026.8	4
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMP HLL	100	B7	56.6	4
1147.05	pol 530	FP HCLAFSYM	95	B7	58.5	5
1359.01	pol 640	YPALMPLYACI	95	B7	1393.4	3
1039.06	env 359	WMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1373.78	pol 166	ASF CGSPY	100	A1	247.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
1069.08	env 249	ILL LCLIFLL	100	A1	192.0	1
20.0269	env 236	RWMCLRRF I I	95	A24	11.0	3
20.0271	pol 392	SWPKFAV PNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.38	core 101	LWFHISCLTF	85	A24	6.7	3
1373.07	core 117	EYLVSF GVV	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

FIG.22A

Inventors: SETTE et al.

Tel. No.: 202-371-2600

For: Optimized Multi-Epitope Constructs and Uses Thereof

57/90

[illegible]

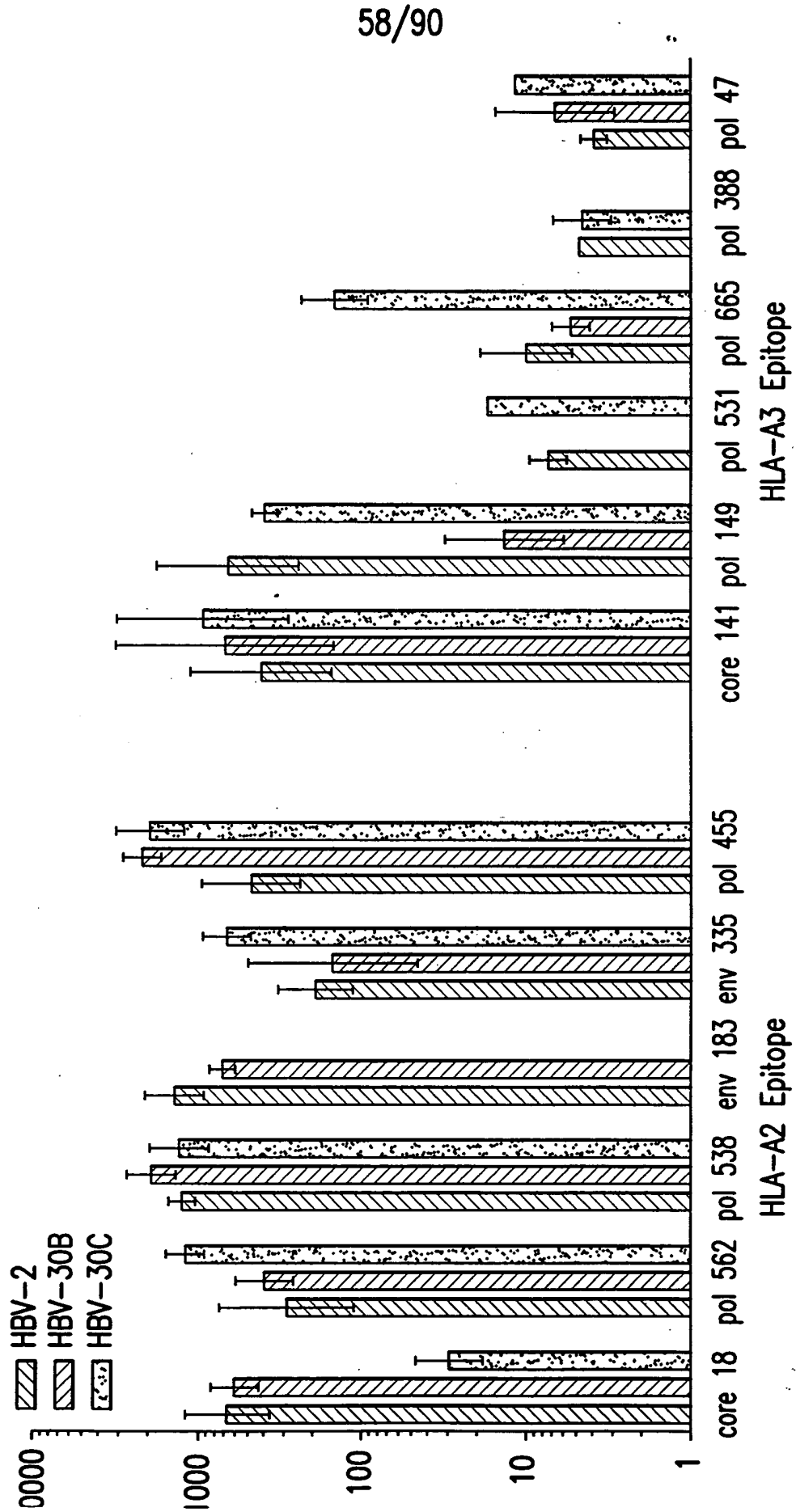


FIG.22C

59/90

HBV-30B

MGMQVQIQSLFLLLLWVPGSRGFLLTRILTINAAASWPKFAVPNLKAAHTLWKAGILYKKADLLDTASALYNQAFIFS
PTYKGAAANVSIPTWKGAFAFLLSLGIHLNIPSSWAFKAAALWFHISCLTFKAAAILLLCLIFLLNAAAYPALMPL
YACINAHPAAMPHLLKAAASFCGSPYKAAGLSRYVARLNKYTSFPWLLNFLPSDFFPVSKAFPHCLAFSYMKAEYLVSF
GVWNAALTFGRETVLEYKAAALPSDFFPVSKAYMDDVVLGVNLVVDVSQFSRNAAARWMLRRFIINAARFSWLSLLVP
FNAATPARVTGGVFKAAWLSLLVPFVNSAICSVVRRKAKFVAAWTLKAAAKWMMWYGPSLYKAASTLPETTVVRRKLS
LDVSAIFY

ATGGGAATGCAGGTCCAGATACAGAGCTTGTTCTCCTCCTGCTTTGGGTCCCCGGATCAAGGGGTTTCCTCCTAACCC
GCATCCTGACAATTAACGCCGAGCCTCCTGGCCAAATTTGCCGTGCCAAATCTCAAGGCAGCTGCACACACACTATG
GAAAGCAGGGATACTGTACAAGAAAGCCGATCTGCTAGACACAGCGTCTGCGTTGTACAACCAGGCTTTTACTTTCTCT
CCTACATATAAAGGCGCAGCTGCAAACGTGAGTATCCCTTGGACGCACAAAGGAGCCGCTGCCAACTTCTTACTGTCCC
TGGGCATCCATCTAAATATCCCTATTCCTTCATCCTGGGCATTTAAAGCAGCCGCCTTATGGTCCACATAAGTTGTCT
GACCTTCAAAGCCGAGCAATCCTGCTCCTTTGCCTCATTTTCTTACTAAACGCCGCTGCCTATCCAGCTCTTATGCCA
TTGTACGCATGTATCAACGCCACCCCGCAGCAATGCCCCACCTCCTTAAAGCTGCCGCCAGTTTCTGCGGTTCTCCTT
ATAAAGCAGCAGGGCTGTCCAGATACGTAGCTAGGCTAAACAAGTATACCAGTTCCTTGGTTACTTAATTTCTGCTCC
GTCAGATTTCTTTCCATCAGTTAAGGCCTTCCCTCATTTGTCTGGCCTTTAGCTACATGAAGGCTGAATATTTGGTATCC
TTCGGCGTGTGGAATGCGGCACTGACATTTGGAAGGGAGACAGTGTCTGAGTACAAAGCCGCCGCACTACCCTCGGACT
TCTTCCCATCGGTCAAAGCTTACATGGACGATGTAGTCTCGGCGTTAACTTAGTAGTGGACTTTTCTCAATTTTCCAG
AAACGCAGCGGCCAGATGGATGTGCCCTTCGGCGTTTTATAATAACGCCGCTCGATTGAGTGGCTATCACTCCTAGTT
CCATTTAATGCAGCTACACCCGCACGGGTGACAGGTGGAGTTTTCAAGGCAGCGTGGCTTTTACTGCTTGTGCCATTTG
TGAACCTCAGCTATTTGCTCAGTAGTGAGAAGGAAGGCAAAATTCGTCGCTGCCTGGACTCTCAAAGCTGCCGCAAAGTG
GATGATGTGGTATTGGGGACCGAGCTTGTACAAAGCGGCCTCTACTCTGCCAGAACTACCGTAGTGAGAAGAAAAGTG
AGCCTGGACGTCAGCGCGGCATTCTACTGA

FIG.22D

HBV-30C

MGMQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAKYTSFPWLLNAAARFSWLSLLVPFNAAPHCLAFSYMKAALVVD
FSQFSRGAILLLCLIFLLNAAHTLWKAGILYKKAWMMWYGPSLYKAYPALMPLYACIGAAWLSLLVPFVNFLTRI
LTINIPSSWAFKAAAEYLVSGVWNLPSDFFPVSKFLPSDFFPVSKDLDTASALYNSWPKFAVPNLKAAASAICSV
VRRKLSLDVSAIFYNAAAKFVAAWTLKAAAKAANVSIPTWKGAAGLSRYVARLNAAASTLPETTVVRRKHPAAMPHLL
KAAARWMLRRFIINASFCSGYKAYMDDVVLGVNALWFHISCLTFKAAATPARVTGGVFKAALTFGRETVLEYKQA
FTFSPTYK

ATGGGAATGCAGGTGCAAATACAGTCTCTTCTTTGCTTCTCTGGGTTCCAGGATCACGGGGCTTCTTGCTTAGCT
TGGGCATCCACCTAAATGCTGCTGCAAAATACACATCTTTTCTTGGCTCCTTAATGCCGCCGCTAGGTTTTCATGGCT
GAGTCTGCTAGTACCTTTCAATGCGGCTTTCCACATTGCCCTAGCTTTTAGCTATATGAAAGCTGCTTTAGTCGTGGAC
TTTTACAGTTTAGCAGAGGAGCAATCCTGCTGCTATGTCTGATATTCCTTCTAAACGCAGCAGCCACACACTCTGGA
AAGCTGGTATCCTTTACAAGAAAGCCTGGATGATGTGGTATTGGGGACCCAGCCTCTACAAAGCATACCCTGCCCTGAT
GCCACTATACGCATGCATTGGCGCGGCAGCCTGGTTATCCCTTTTAGTACCGTTTGTCAACTTTTCTATTAACCAGAATC
CTGACGATTAATATTCGATCCCAAGTTCTTGGGCATTTCAAAGCAGCCGCGGAGTATCTGGTTTCATTTGGCGTATGGA
ACCTGCCAAGCGACTTCTTTCTTCTGTTAAGTTCTTCCCTCCGATTTCTTTCCATCGGTGAAAGACCTCCTTGATAC
CGCGAGCGCTCTGTACAACTCGTGGCCAAATTCGCAGTTCCAAACCTAAAAGCCGCCGCCAGTGCCATTTGTTCCGTG
GTAAGGAGAAAAATTACTCGACGTGTCCGCAGCATTTTATAACGCTGCTGCAAAGTTTGTGCGCAGCATGGACATTGA
AGGCTGCAGCGAAAGCAGCAAATGTATCAATACCTGGACCCACAAGGGTGCAGCCGGGCTGTCTAGGTATGTGGCGAG
GCTAAACGCCGCCGCTCAACACTGCCTGAGACTACTGTCTGAGACGCAAAACACCTGCCGCAATGCCCCACCTGCTG
AAAGCAGCCGCACGATGGATGTGCCCTCAGAAGATTCAATAAACGCTTCTTTCTGTGGGTACCCCTACAAAGCCGCTT
ACATGGACGATGTGGTCTCGGAGTGAATGCCCTCTGGTTCATATCAGCTGCCTGACATTCAAGGCAGCCGCCACCCC
CGCTCGTGTGACAGGAGGTGTCTTCAAAGCCGCCGCACTGACTTTCTGGTCCGGGAACTGTATTGGAATATAAGCAGGCC
TTCACATTCTCCCAACATACAAGTGA

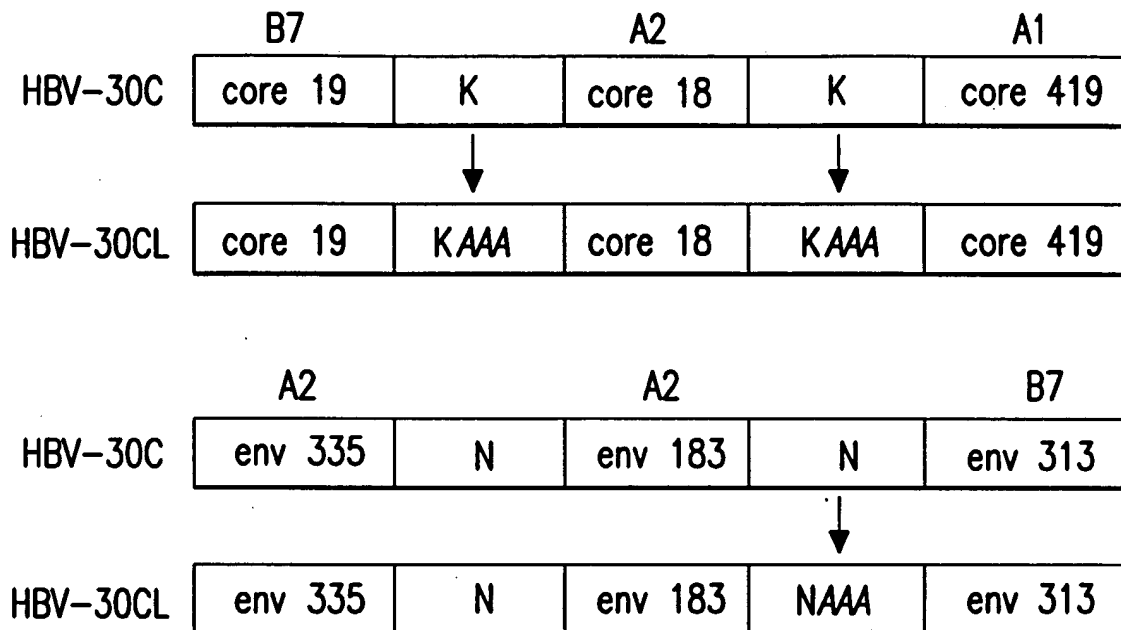


FIG.23A

61/90

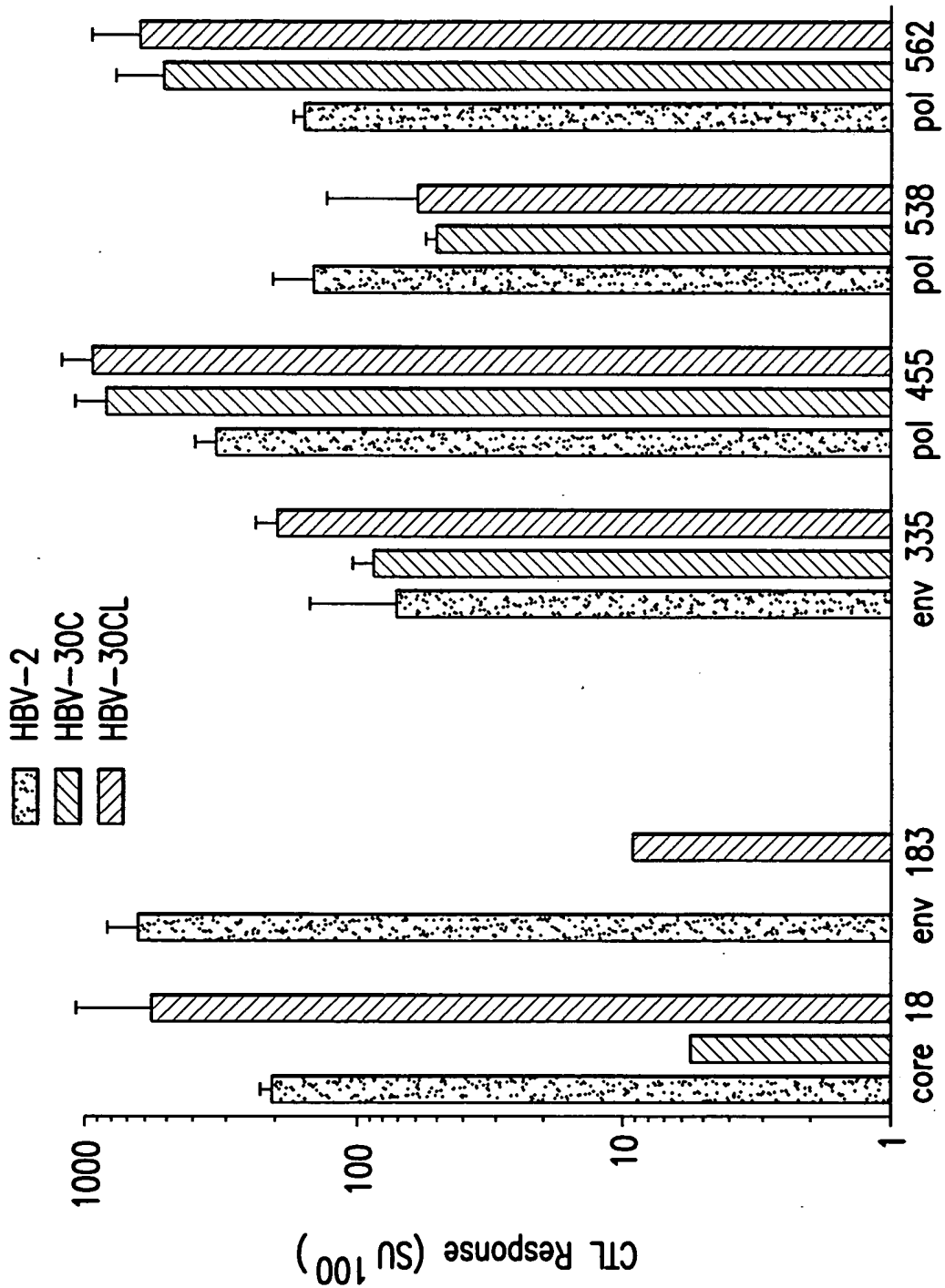


FIG. 23B

62/90

HBV-CL

MQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFSWLSLLVPFNAAFPHCLAFSYMKA
ALVVDIFSQFSRGAILLLCLIFLLNAAHTLWKAGILYKKAWMMWYWGPSLYKAYPALMPYACIGAAWLSL
LVPFVNFLLTRILTINAAAIPISSWAFKAAAEYLVSGVWNLPSDFFPSVKAAAFPSDFPSVKAAADLL
DTASALYNSWPKFAVPNLKAAASAICSVVRRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGA
AGLSRYVARLNAAASTLPETTIVRRKHPAAMPHELLKAAARWMLRRFIINASFCGSPYKAAYMDDVVLGVNA
LWFHISCLTFKAAATPARVTGGVFKAAALTFGRETVLEYKQAFTFSPYK

ATGGGAATGCAGGTGCAAATACAGTCTCTCTTCCTTTTGCTTCTCTGGGTTCCAGGATCACGGGGCTTCTTG
CTTAGCTTGGGCATCCACCTAAATGCTGCTGCAAATACACATCTTTTCCTTGGCTCCTTAATGCCGCCGCT
AGGTTTTTCATGGCTGAGTCTGCTAGTACCTTTCAATGCGGCTTTCCACATTGCCTAGCTTTTAGCTATATG
AAAGCTGCTTTAGTCGTGGACTTTTCACAGTTTAGCAGAGGAGCAATCCTGCTGCTATGTCTGATATTCCTT
CTAAACGCAGCAGCCACACACTCTGGAAAGCTGGTATCCTTTACAAGAAAGCCTGGATGATGTGGTATTGG
GGACCCAGCCTCTACAAAGCATACCCTGCCCTGATGCCACTATACGCATGCATTGGCGCGGCAGCCTGGTTA
TCCCTTTTAGTACCGTTTGTCAACTTTCTATTAACCAGAATCCTGACGATTAATGCTGCCGCCATTCCGATC
CCAAGTTCCTGGGCATTCAAAGCAGCCGCGGAGTATCTGGTTTCATTTGGCGTATGGAACCTGCCAAGCGAC
TTCTTTCCTTCTGTAAAGCCGCTGCTTTCCTCCCCTCCGATTTCTTTCATCGGTGAAAGCCGCTGCCGAC
CTCCTTGATACCGGAGCGCTCTGTACAACTCGTGGCCAAAATTCGCAGTTCCAAACCTAAAAGCCGCCGCC
AGTGCCATTTGTTCCGTGGTAAGGAGAAAAATTATCACTCGACGTGTCCGCAGCATTTTATAACGCTGCTGCA
AAGTTTGTGCGCAGCATGGACATTGAAGGCTGCAGCGAAAGCAGCAAATGTATCAATACCCTGGACCCACAAG
GGTGCAGCCGGGCTGTCTAGGTATGTGGCGAGGCTAAACGCCGCCGCTCAACACTGCCTGAGACTACTGTC
GTGAGACGCAAACACCCTGCCGCAATGCCCCACCTGCTGAAAGCAGCCGCACGATGGATGTGCCTCAGAAGA
TTCATAATAAACGCTTCTTCTGTGGGTACCCTACAAAGCCGCTTACATGGACGATGTGGTCTCGGAGTG
AATGCCCTCTGGTTCCATATCAGCTGCCTGACATTCAAGGCAGCCGCCACCCCGCTCGTGTGACAGGAGGT
GTCTTCAAAGCCGCGGCACTGACTTTCGGTCGGGAAACTGTATTGGAATATAAGCAGGCCTTCACATTCTCC
CCAACATACAAGTGA

FIG.23C

Epitope	# DR	HLA-DR Binding Capacity (IC50 nM)															
		DRB1*0101	DRB1*1501	DRB1*0301	DRB1*0401	DRB1*0405	DRB1*1101	DRB1*1201	DRB1*1302	DRB1*0701	DRB1*0802	DRB1*0901	DRB5*0101	DRB3*0101	DRB4*0101		
pol 412	10	2.0	21	-	10.0	47	303	397	143	173	598	791	1067	1837	4179		
pol 664	11	10	41	-	88	181	82	-	190	90	416	142	144	4848	322		
env 180	10	1	217	-	9	258	6	4229	9	8	189	56	1158	4374	696		
pol 774	9	15	748	-	119	94	443	-	-	94	818	220	400	-	-		
core 120	8	27	43	-	58	220	11	817	565	78	76	1773	7	6454	395		
pol 145	10	17	4.0	-	2271	1499	42	149	766	61	36	133	35	-	782		
env 339	9	408	14	-	315	28	54	452	2330	2744	60	31	1516	1661	22		
pol 501	8	248	558	-	77	244	492	9462	-	-	800	1551	560	-	102		
pol 523	7	27	359	-	560	246	1749	-	59	328	940	1373	4764	-	1347		
pol 618	6	3.0	4370	-	40	34	1617	-	821	62	872	5175	1246	-	3060		
pol 767	8	55	386	-	966	1634	1520	802	143	44	214	299	3276	-	6553		
core 50	7	810	8.0	-	326	-	458	-	-	676	210	952	124	575	48		
pol 694	2	7470	5009	67	490	1203	-	-	2022	-	-	-	-	1808	1044		
pol 385	3	7372	1368	36	208	251	-	-	946	-	-	-	-	2525	8711		
pol 96	1	8415	4153	43	3916	1908	6666	-	4461	-	5354	-	4330	-	8121		
pol 420	4	38	3089	62	168	17	4923	1859	36	5063	1065	7126	-	5	7		

FIG.24A

64/90

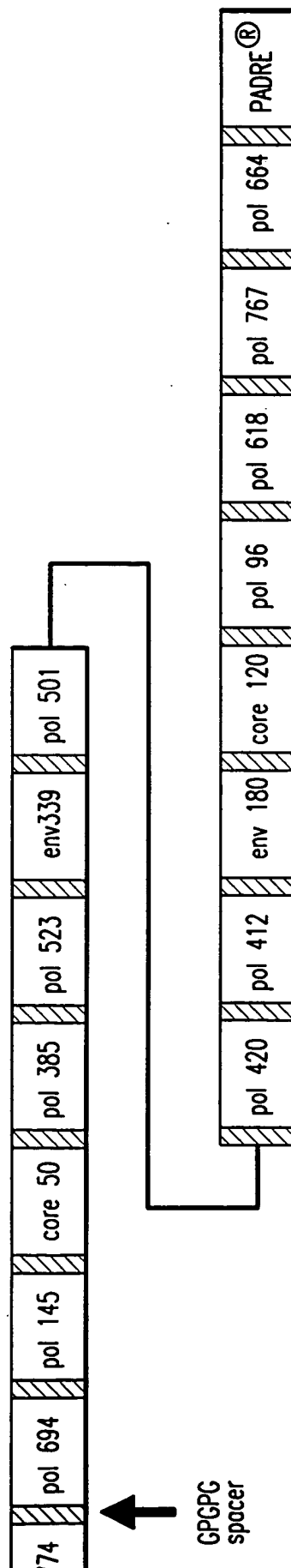


FIG. 24B

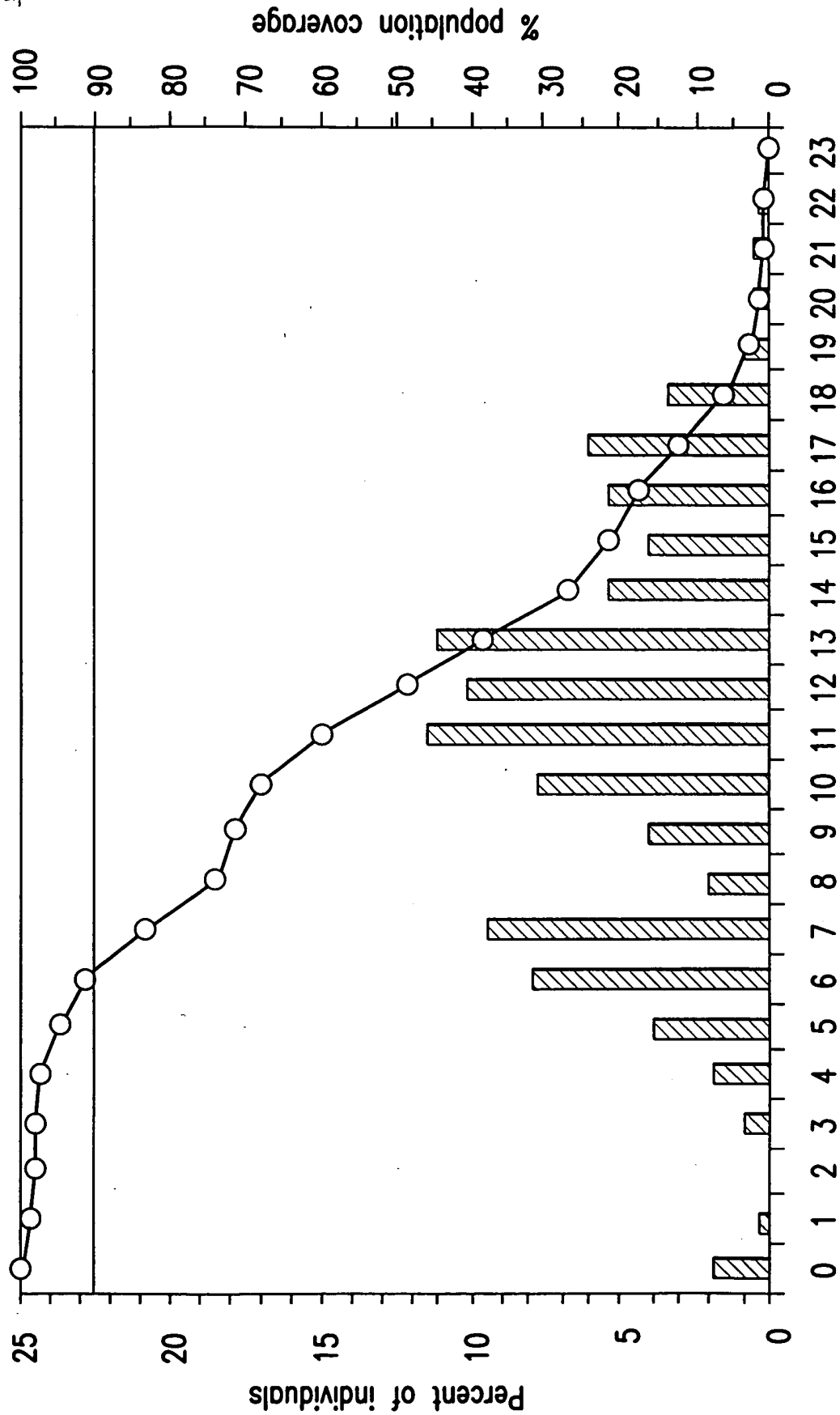
HBV-HTL

MGTSFVYVPSALNPADGPGPGLCQVFADATPTGWGLGPGPGRHYLHTLWKAGILYKGP GPGPHHTALRQAILC
WGELMTLAGPGPGESRLVVD FSQFSRGN GPGPGPFLLAQFTSAICSVVGP GPGPLVPFVQWFVGLSPTVGP GPG
LHLYSHPIILGFRKIGPGPGSSNLSWLSLDVSAAFGPGPGLQSLTNLLSSNLSWLGPGPGAGFFLLTRILTIP
QSGPGPGVSFGVWIRTPPAYRPPNAPIGPGPGVGPLTVNEKRRLKLIGPGPGKQCFRKL PVNRPIDWGP GPGA
ANWILRGTSFVYVPGPGPGKQAF TFSPTYKAFLCGPGPGA KFVAAWTLKAAA

ATGGGAAC TTTCTTTTGTGTATGTCCCTTCCGCTCTGAACCCAGCAGACGGACCCGGGCCTGGCCTGTGCCAGG
TCTTCGCCGACGCAACTCCACAGGGTGGGGGCTGGGGCCAGGACCAGGCAGGCACTACCTGCATACTCTGTG
GAAGGCAGGAATCCTCTATAAAGGGCCCGGCCAGGCCCTACCACACCGCCCTGAGGCAGGCCATCCTGTGC
TGGGGGGAGCTCATGACCCTGGCCGGACCTGGACCCGGGGAGAGCAGACTGGTGGTGGATTT CAGCCAATTCA
GCAGAGGAAACGGACCCGGCCCTGGGCC TTTTCTGCTGGCTCAGTTTACATCTGCTATTTGTTCTGTGGTCGG
CCCCGGGCCCGGACTCGTGCC TTTCTGTGCAGTGGTTCGTGGGACTGTCCCTACAGTCGGGCCCGGCCAGGG
CTGCATCTGTACTCCCAACCAATCATCTCGGCTTCCGCAAGATTGGACCCGGCCAGGCTCCAGCAATCTCT
CCTGGCTCTCTCTGGACGTGTCTGCCGCCTTTGGCCCTGGACCAGGCCTGCAAAGCCTGACTAATCTGCTCAG
CAGCAACCTGTCCTGGCTGGGACCTGGCCCAGGGGCTGGCTTCTTTCTGCTCACCCGGATTCTCACAATTCCC
CAGTCCGGACCAGGACCAGGAGTCAGTTTCGGGGTGTGGATCAGGACCCCTCCTGCTTATAGACCACCCAATG
CTCCAATCGGCCCGGCCCTGGCGTCGGGCCACTGACCGTGAATGAGAAGCGCCGGCTGAAGCTGATCGGCC
TGGCCCTGGCAAGCAGTGCTTT CGCAAAC TGGCGTGAACAGACCTATTGATTGGGGCCCCGGCCCTGGAGCA
GCCAACTGGATTCTCAGGGGAACAAGCTTCGTCTACGTGCCCGGGCCCGGACCAGGGAAGCAGGCTTTTACCT
TCTCTCCCACTTACAAGGCCTTCCTCTGTGGGCCAGGCCCGGCCCAAGTTTGTGGCAGCATGGACCCTCAA
AGCCGCTGCCTGA

FIG.24C

66/90



No. epitopes recognized

FIG. 25A

67/90

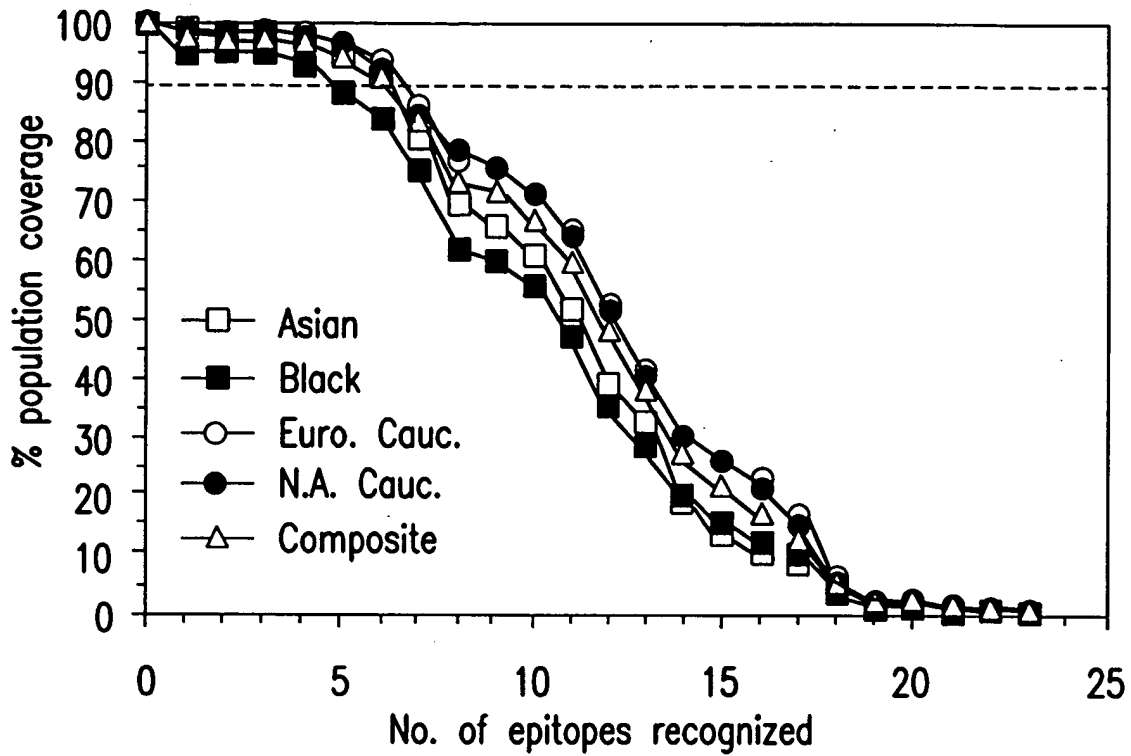


FIG.25B

68/90

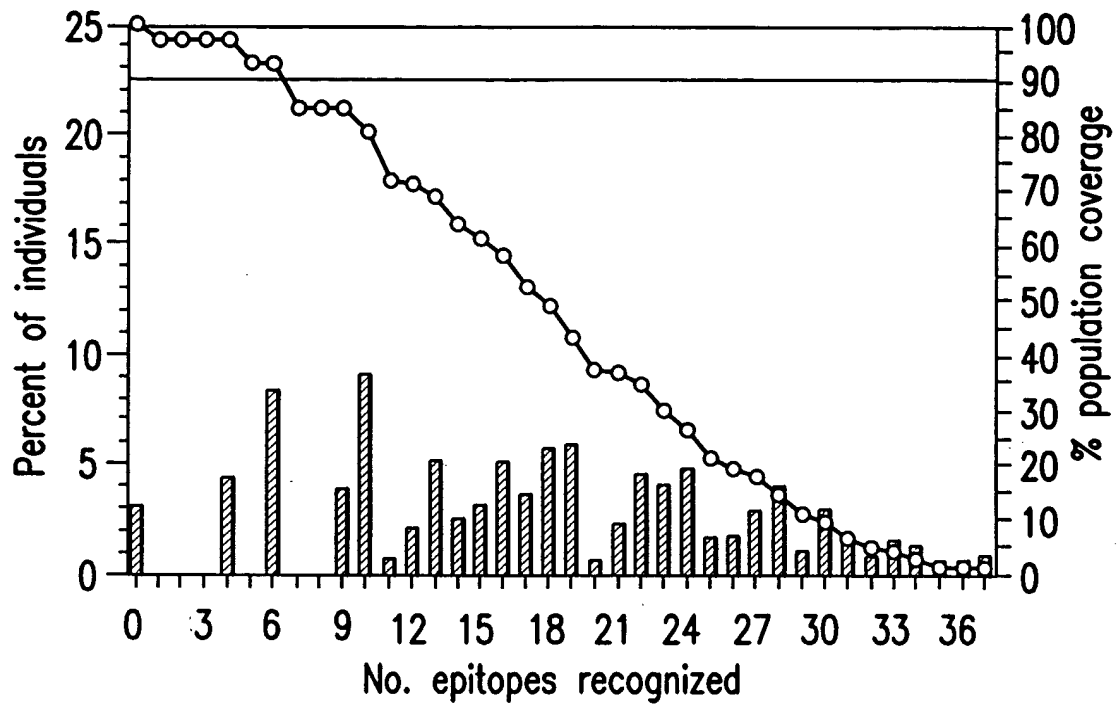


FIG. 26A

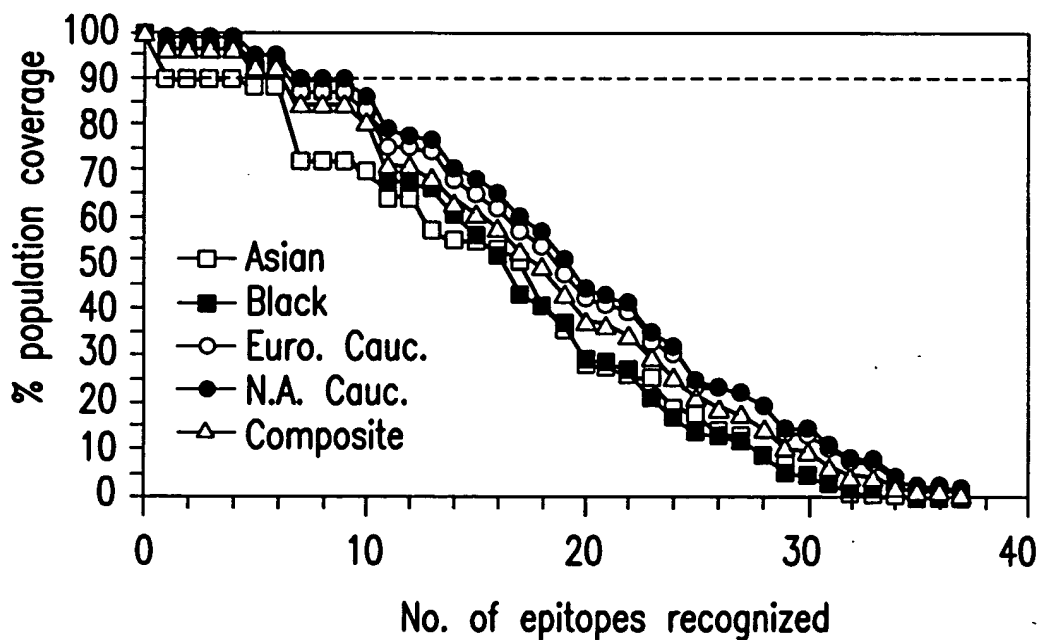


FIG. 26B

69/90

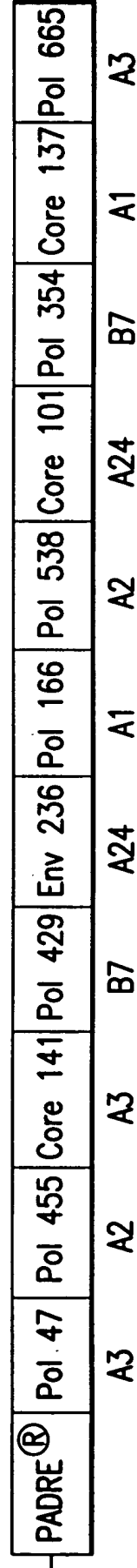
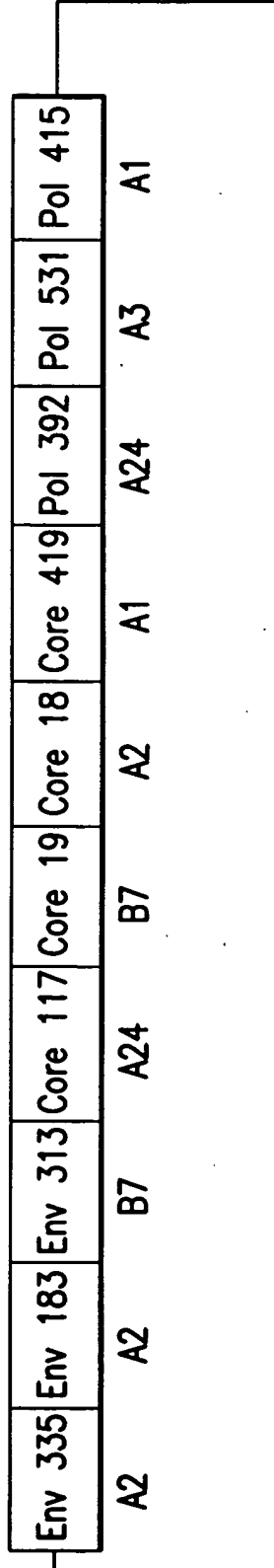
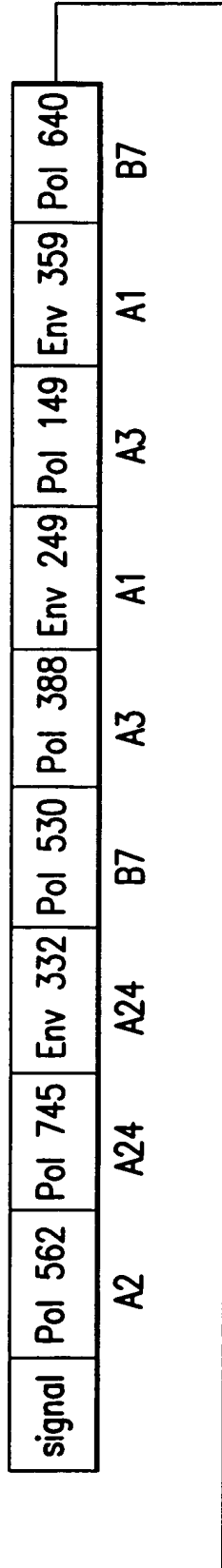


FIG. 27A

70/90

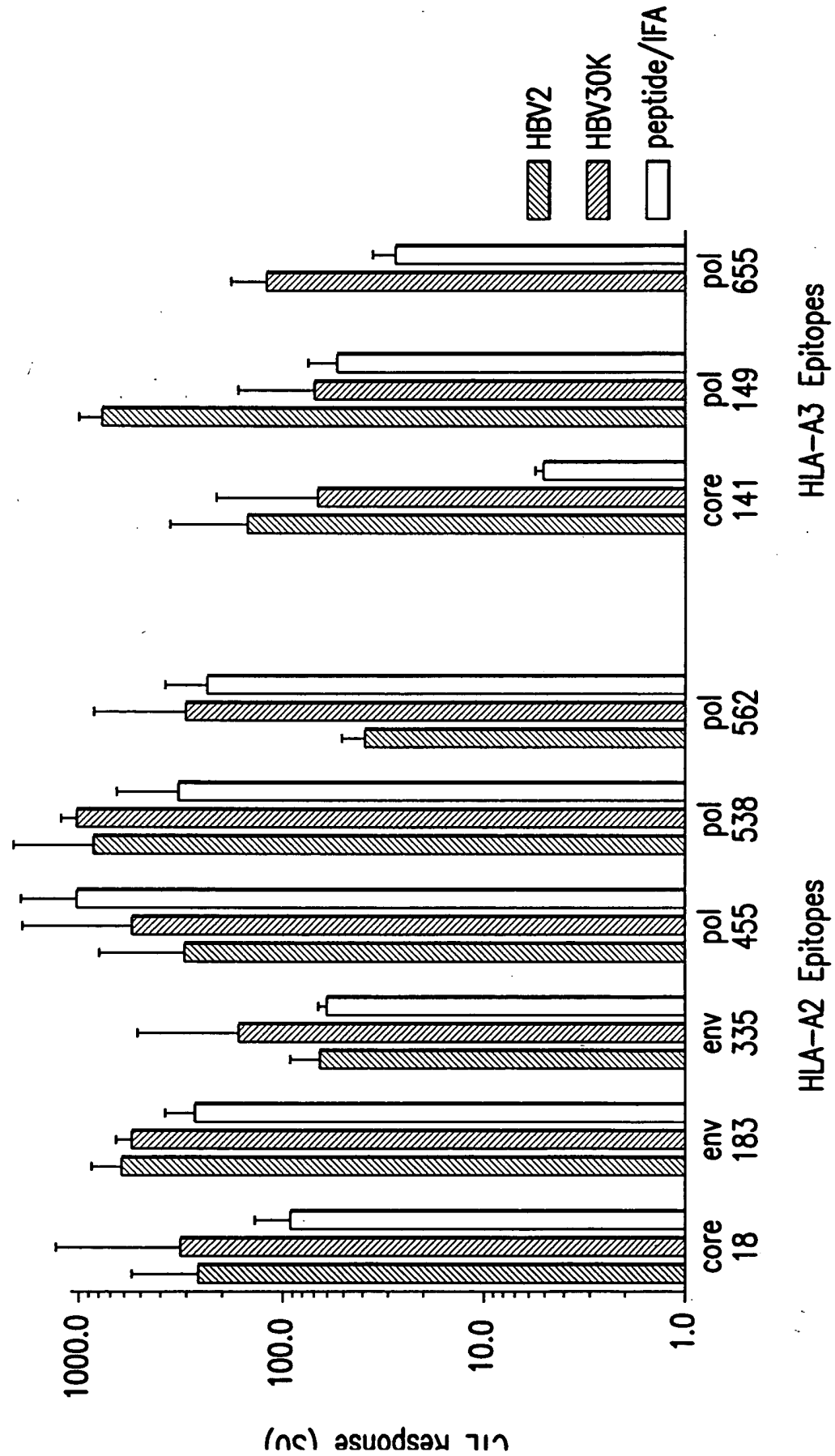


FIG.27B

71/90

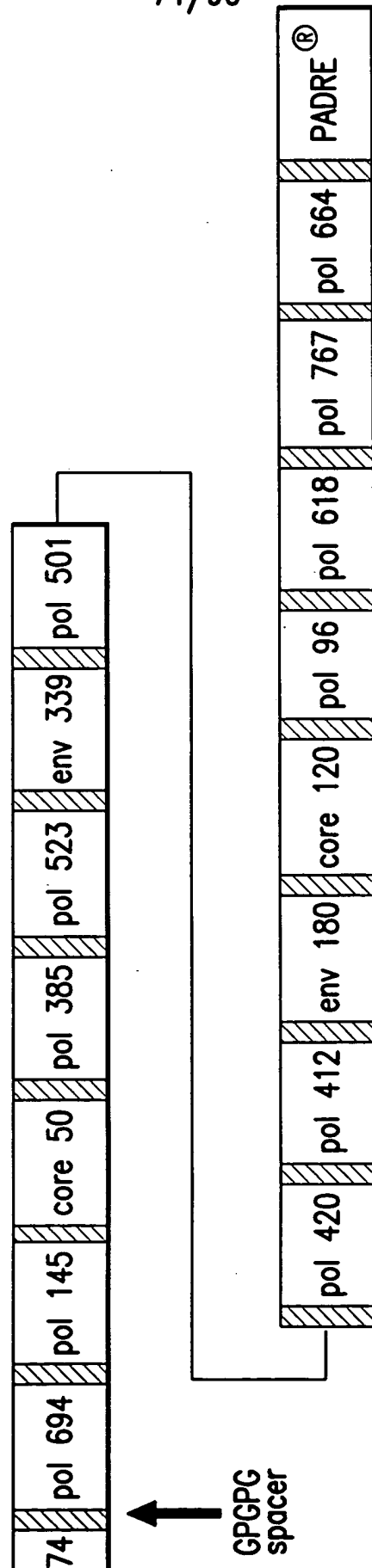


FIG. 28A

72/90

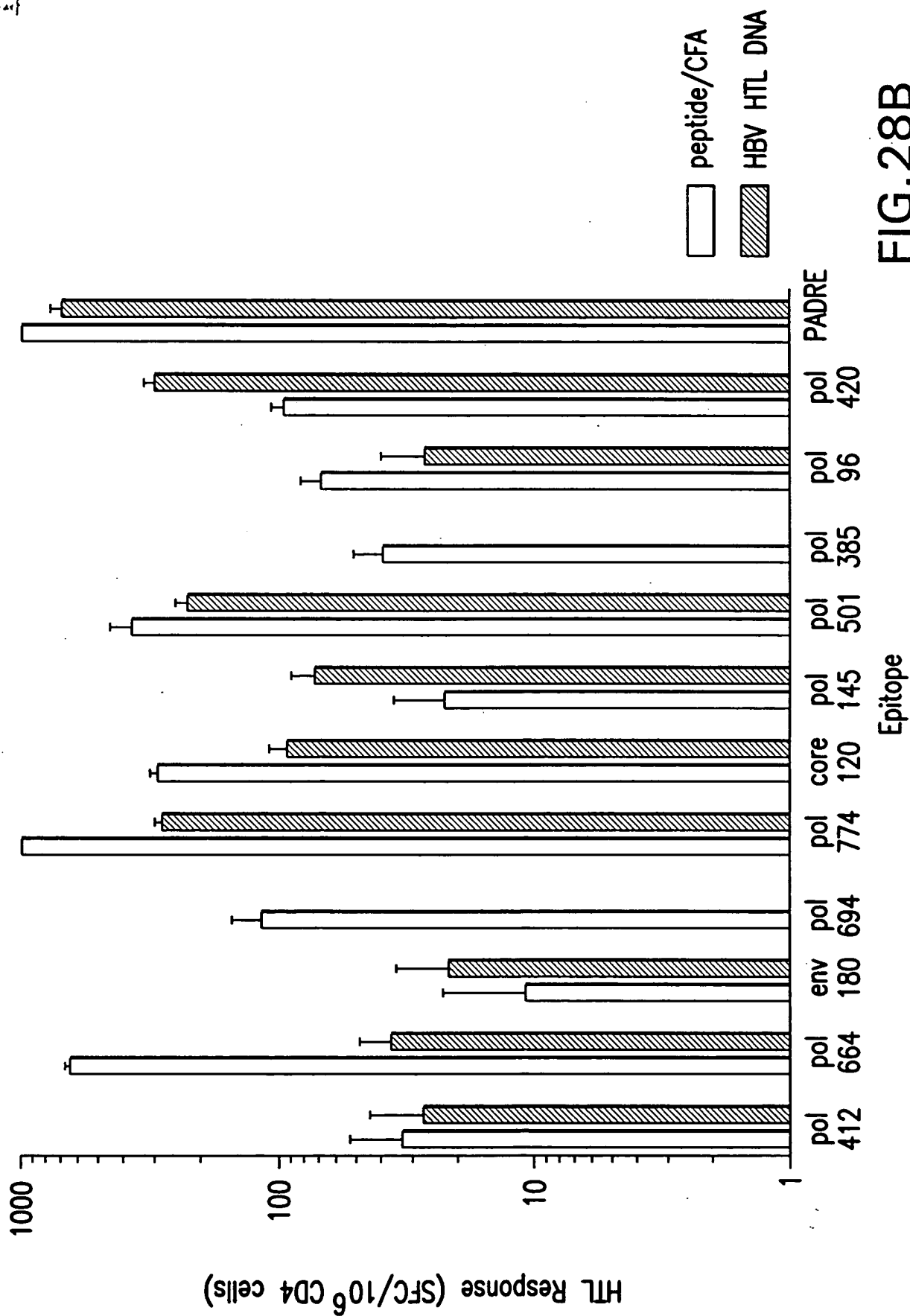


FIG. 28B

73/90

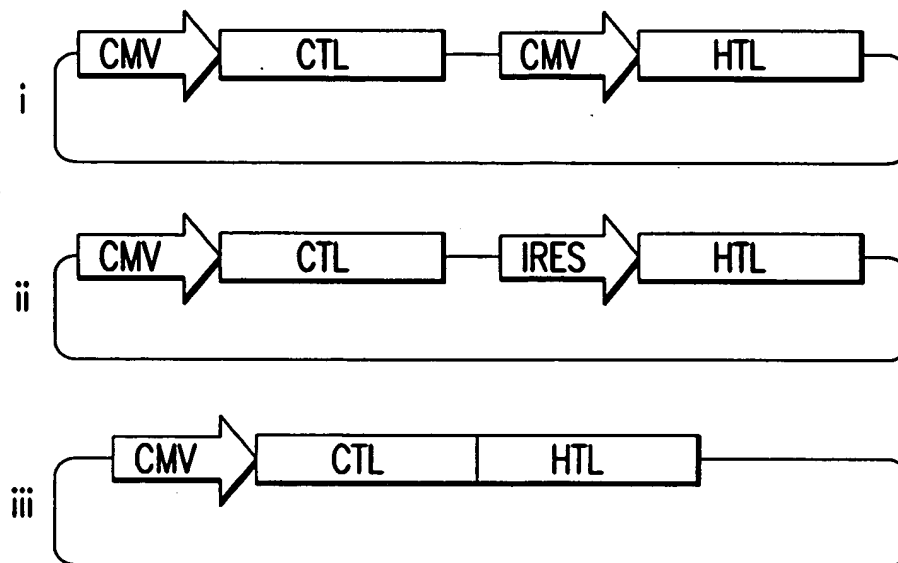


FIG.29A

74/90

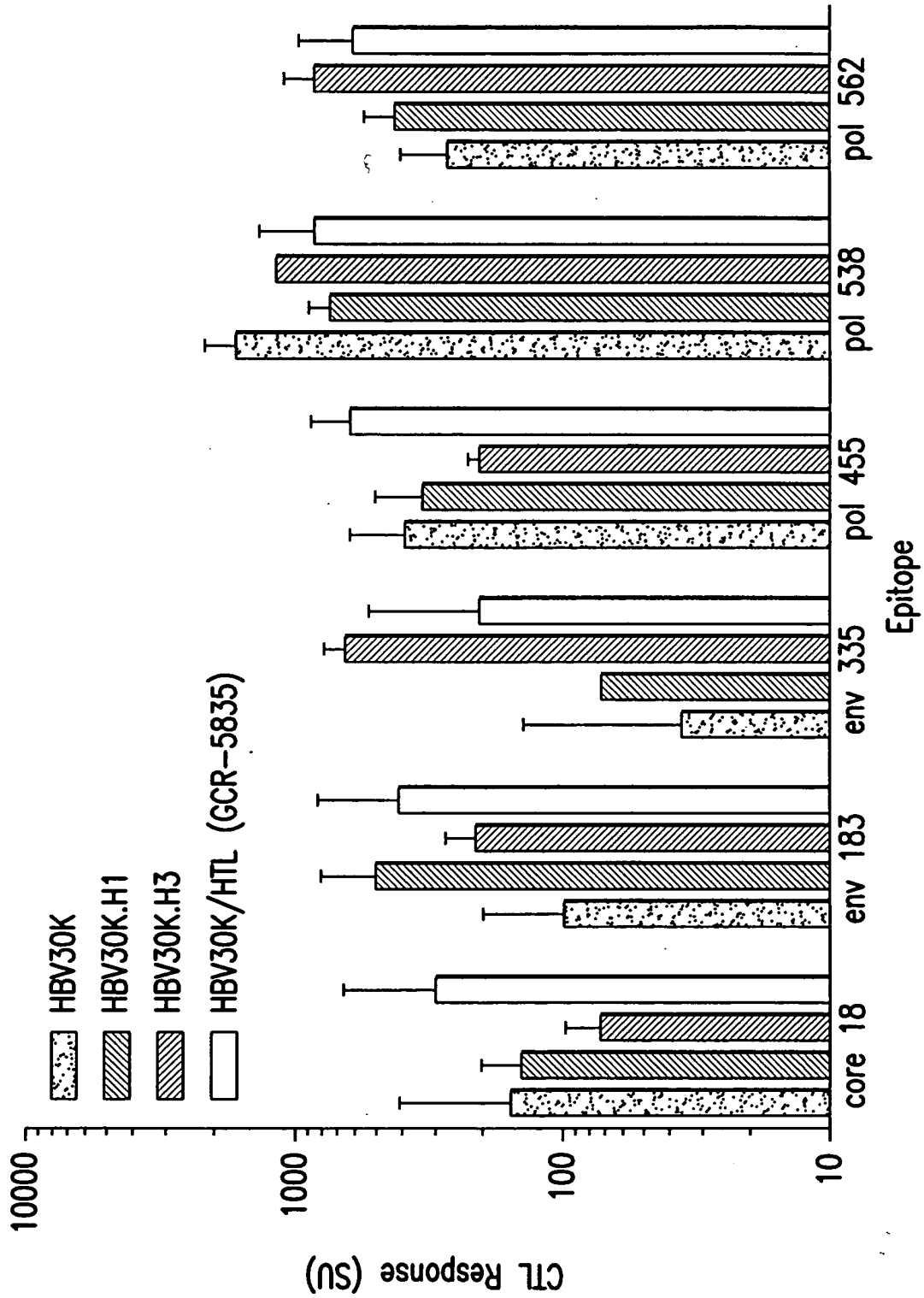


FIG.29B

75/90

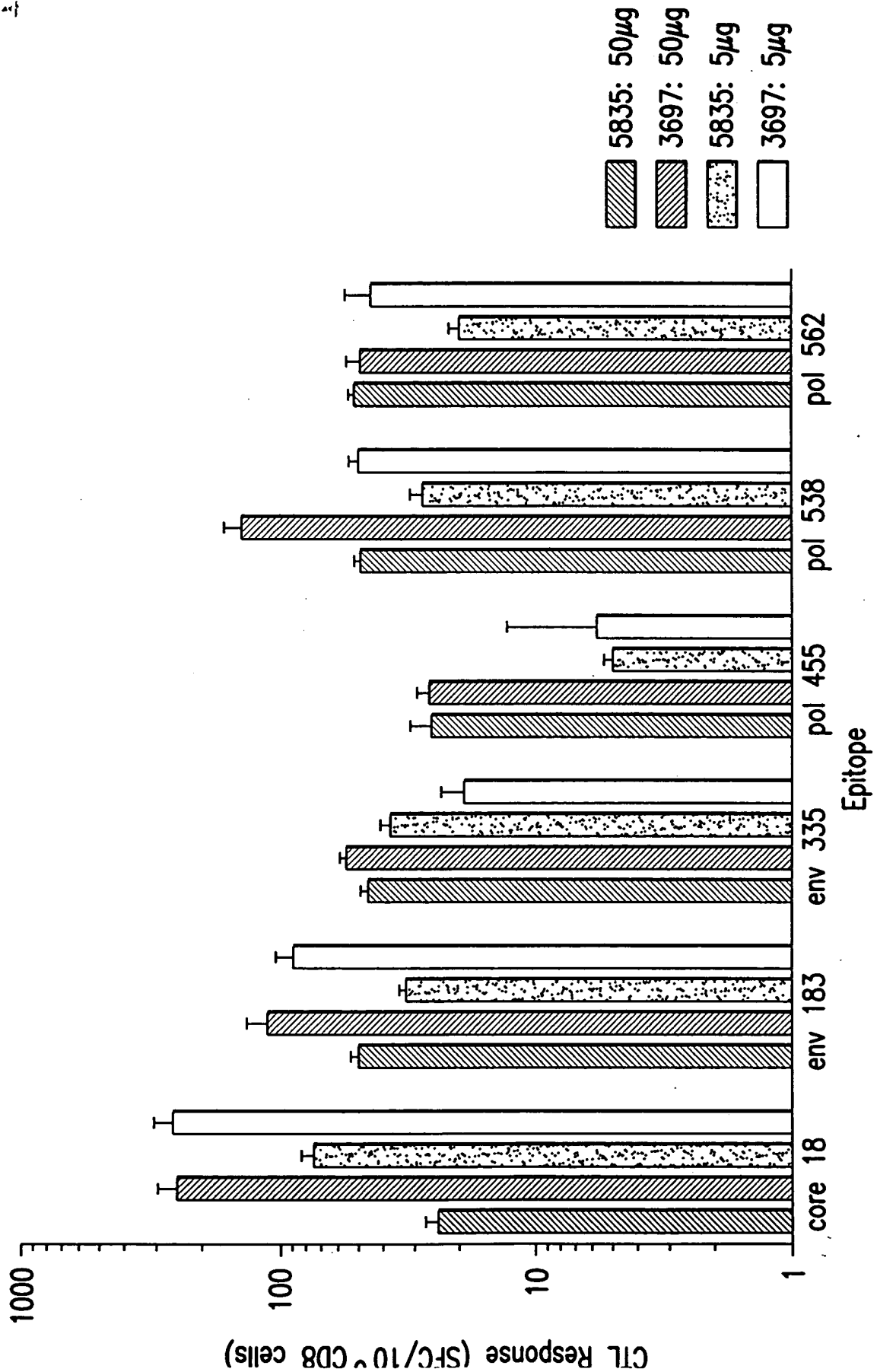
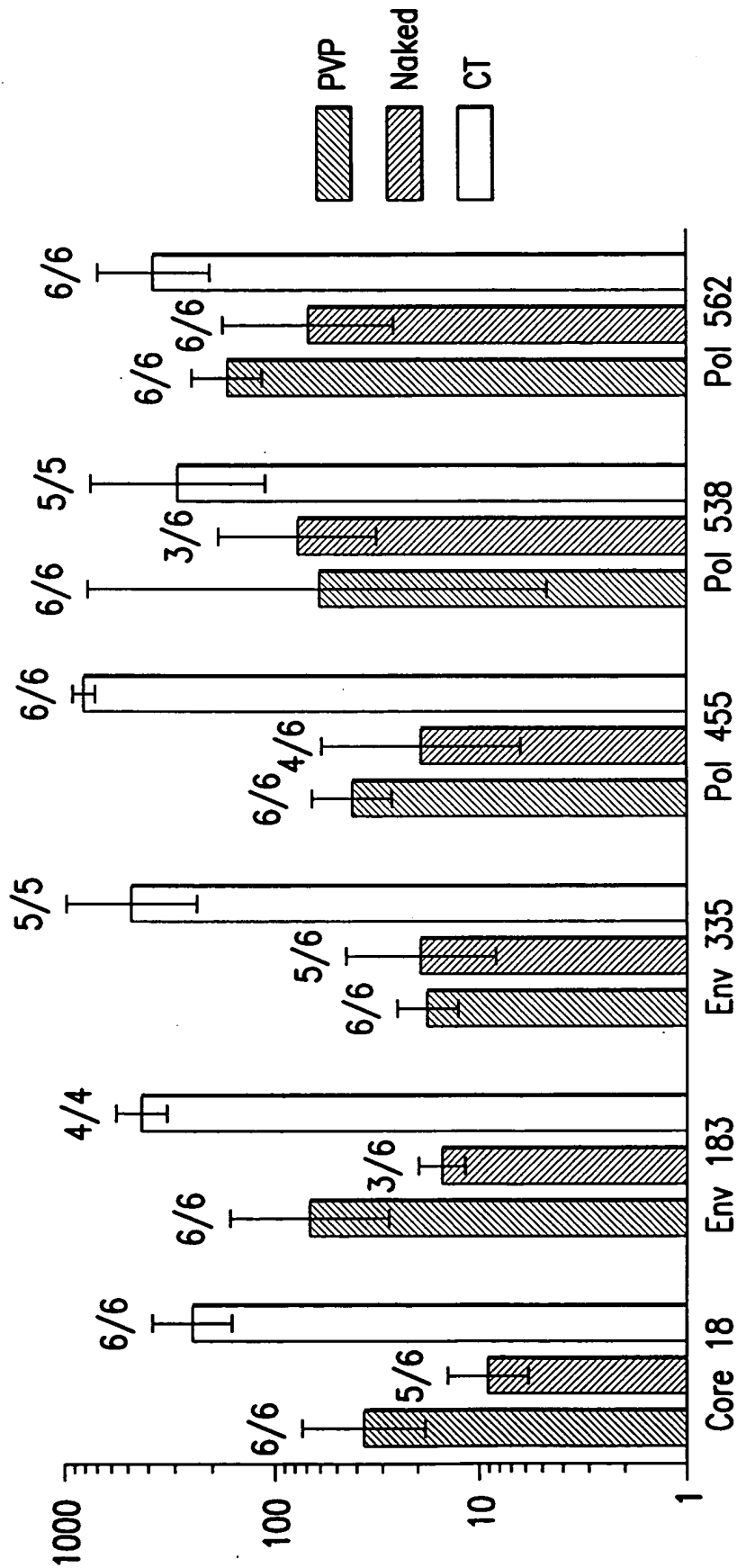


FIG.30

76/90



Epitope
 FIG.31

77/90

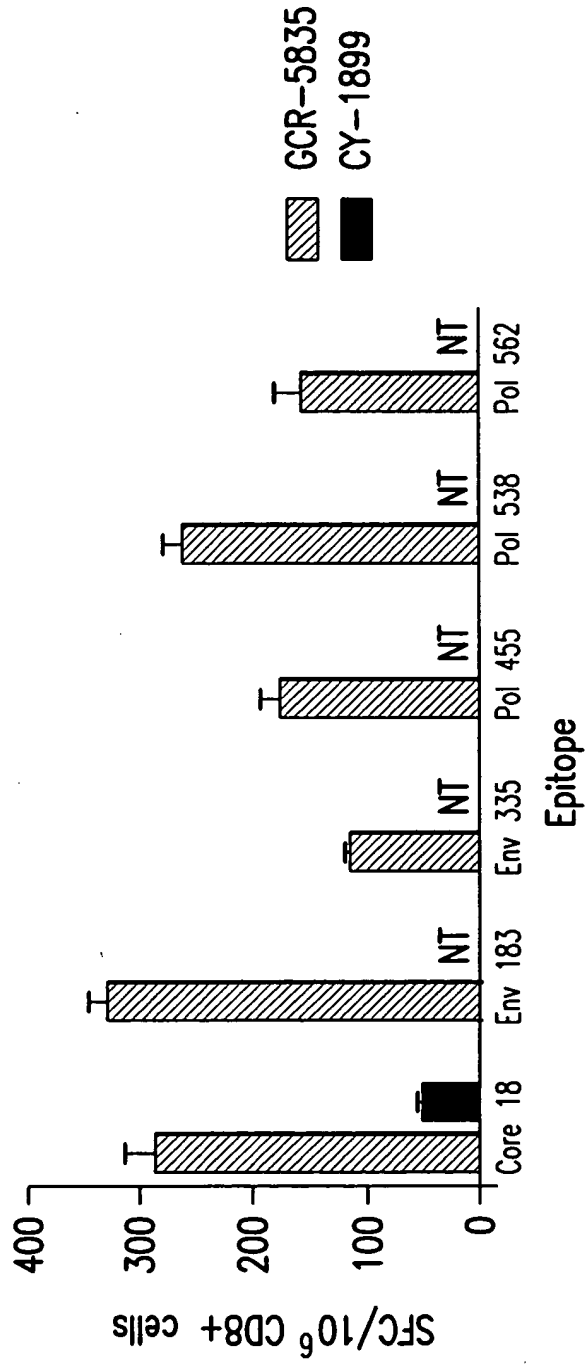


FIG. 32A

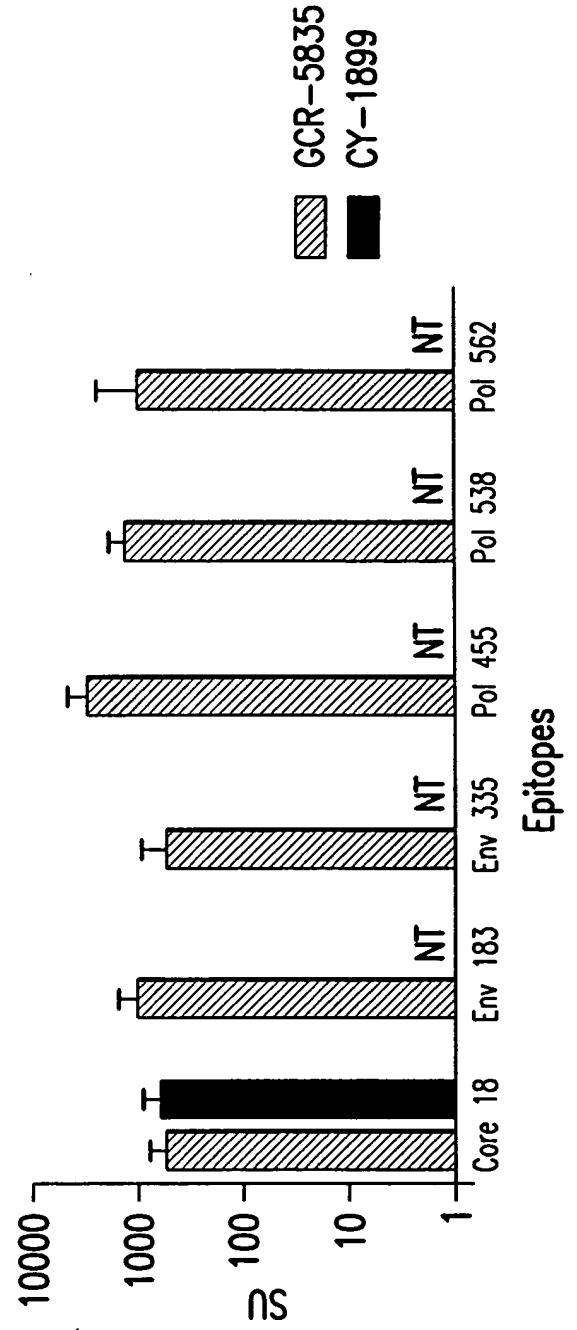


FIG. 32B

78/90

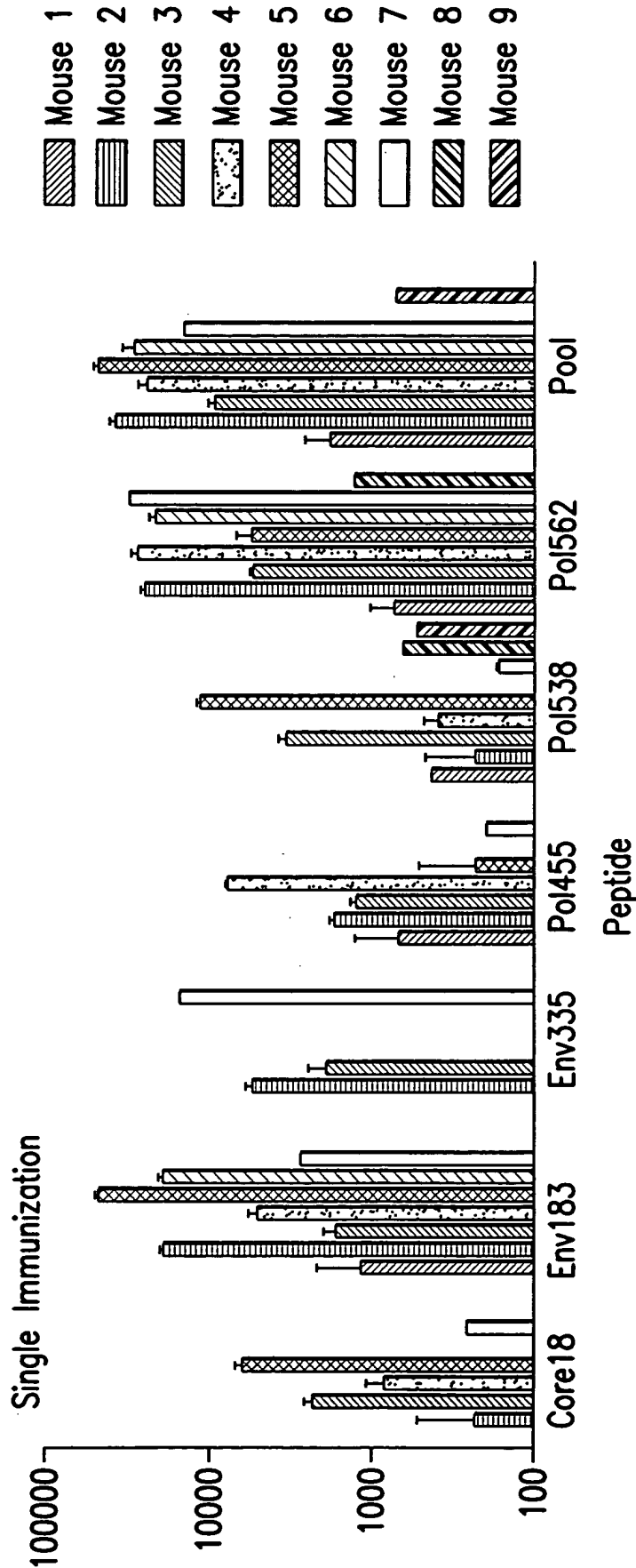


FIG. 33A

79/90

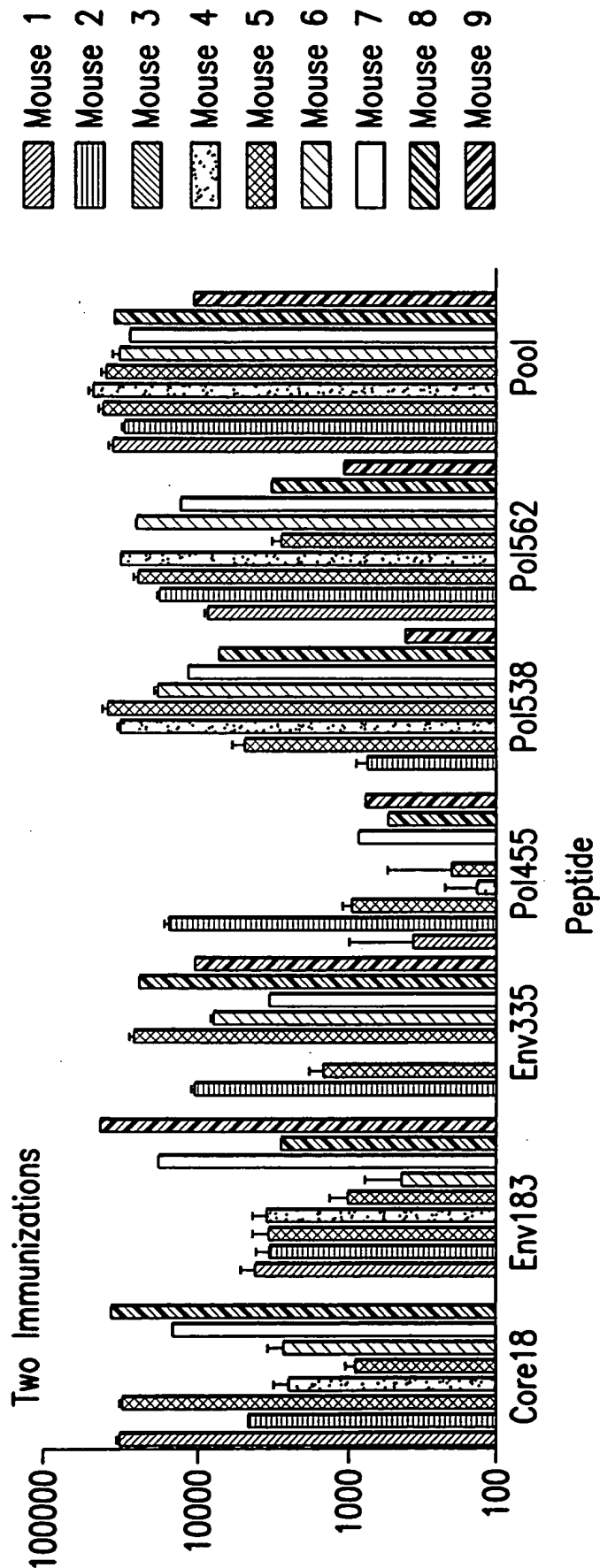
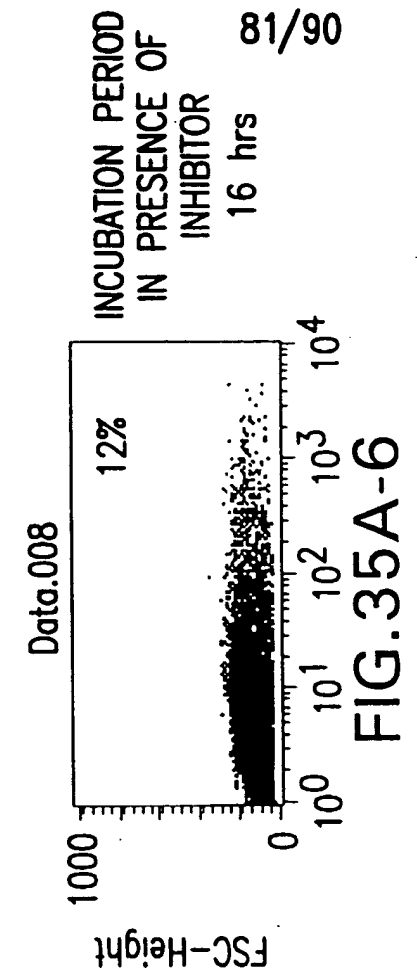
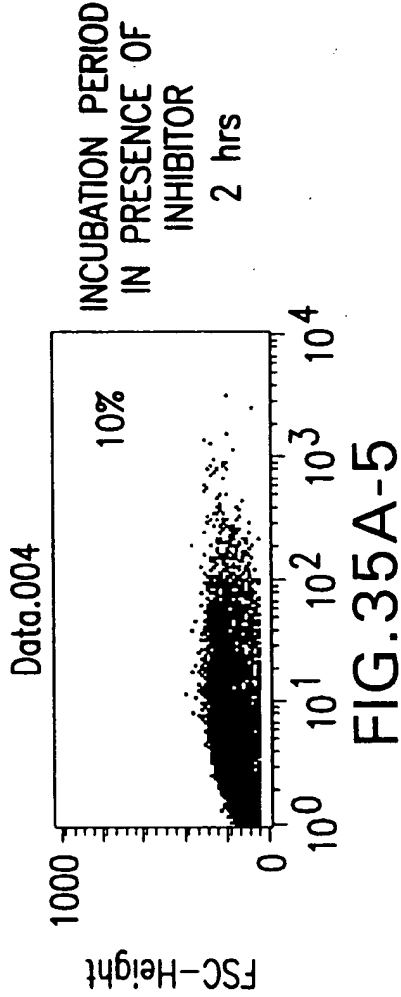
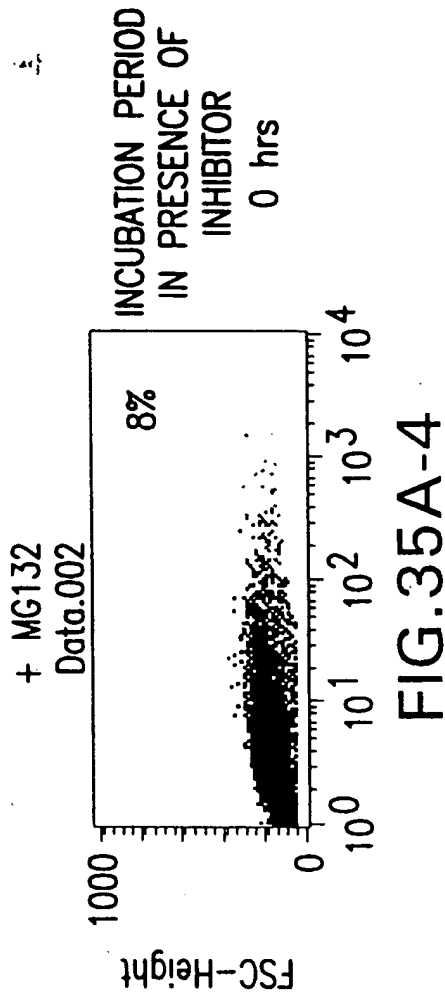
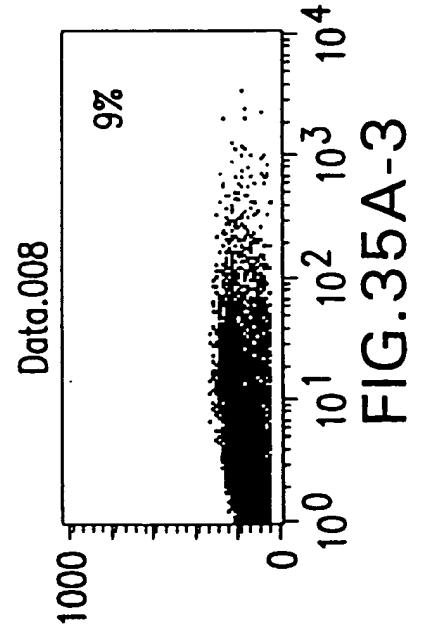
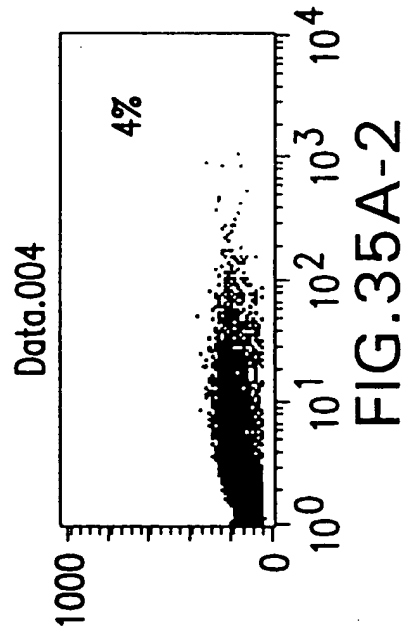
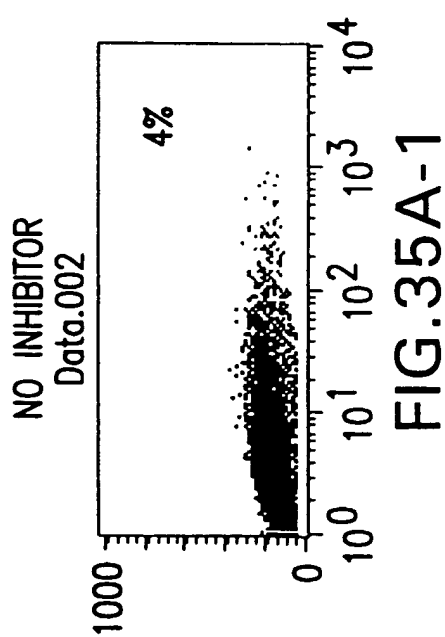


FIG. 33B

[illegible]

FIG. 34



82/90

Detection of HBV AOSIb
(un-optimized epitope string)
-MG132

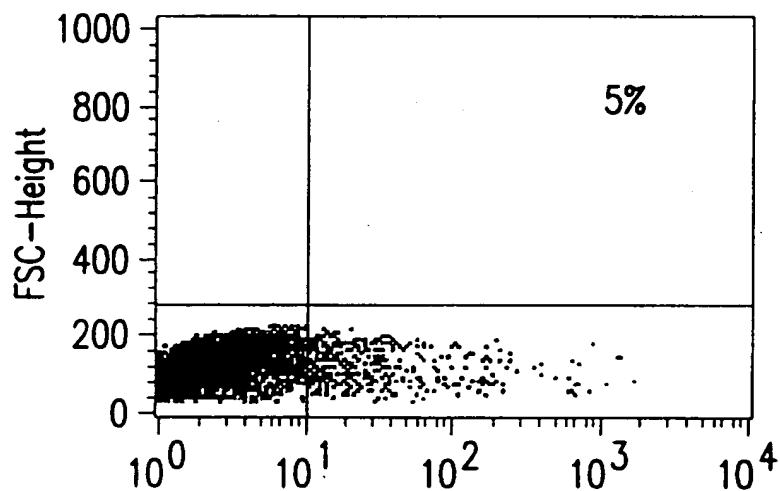


FIG.35B-1

Detection of HBV AOSIb
(un-optimized epitope string)
+MG132

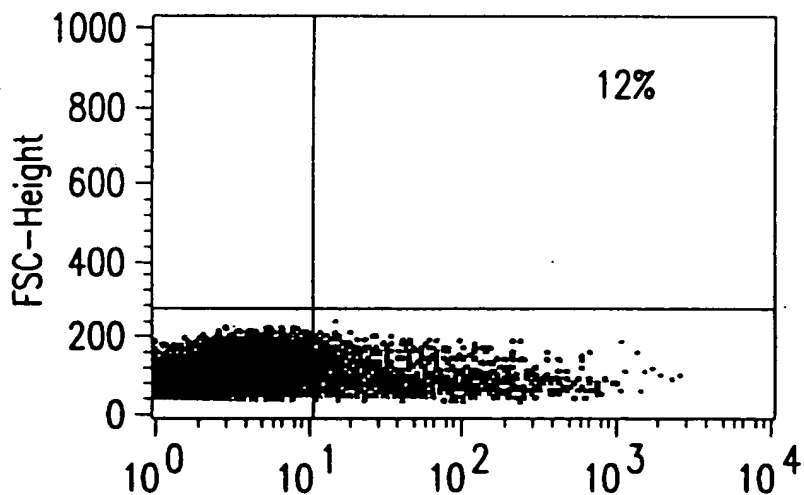


FIG. 35B 2

84/90

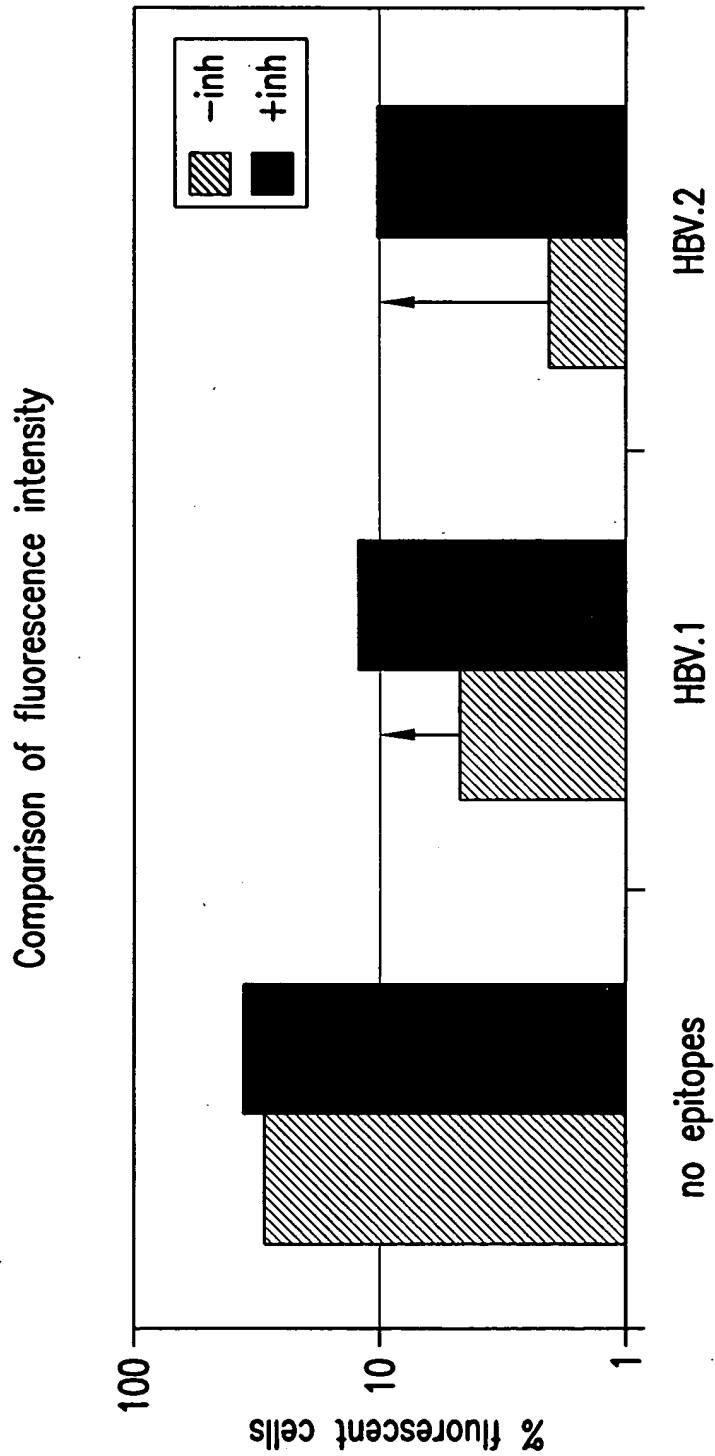


FIG.35D

85/90

plasmid	No inhibitor	with inhibitor	Fold Increase (aver.)
Fluorescent Protein (no epitopes control)	30% 34%	35% 33%	1.1
HBV AOSIb fusion	5% 4.4	12% 8%	2.1
HBV AOSIb2 fusion	2% 1.2%	10% 6.6	5.3

FIG.35E

86/90

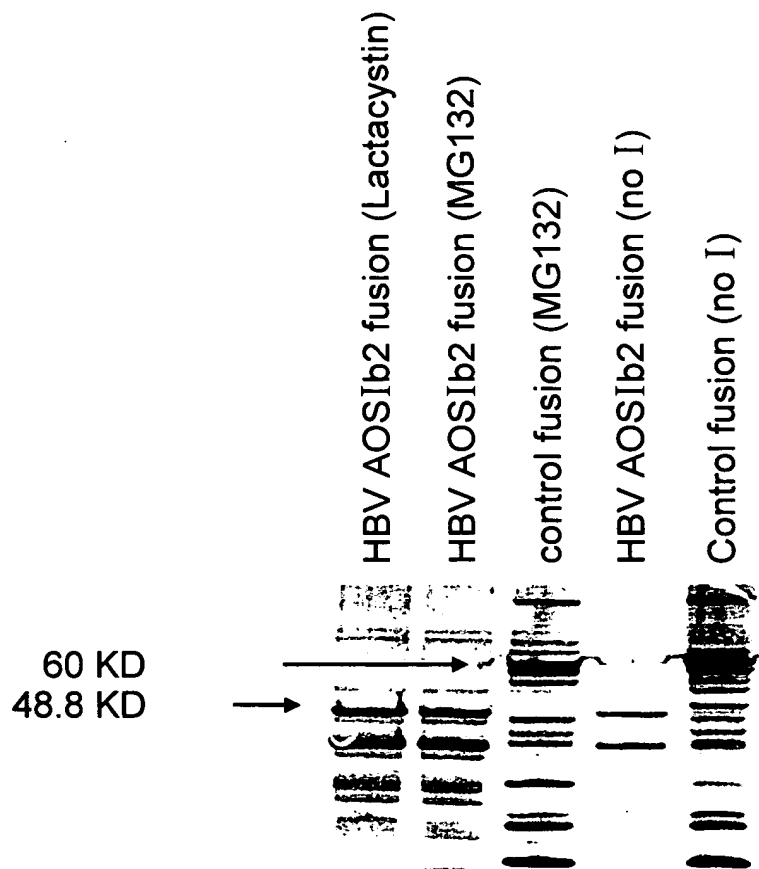


FIG.36

87/90

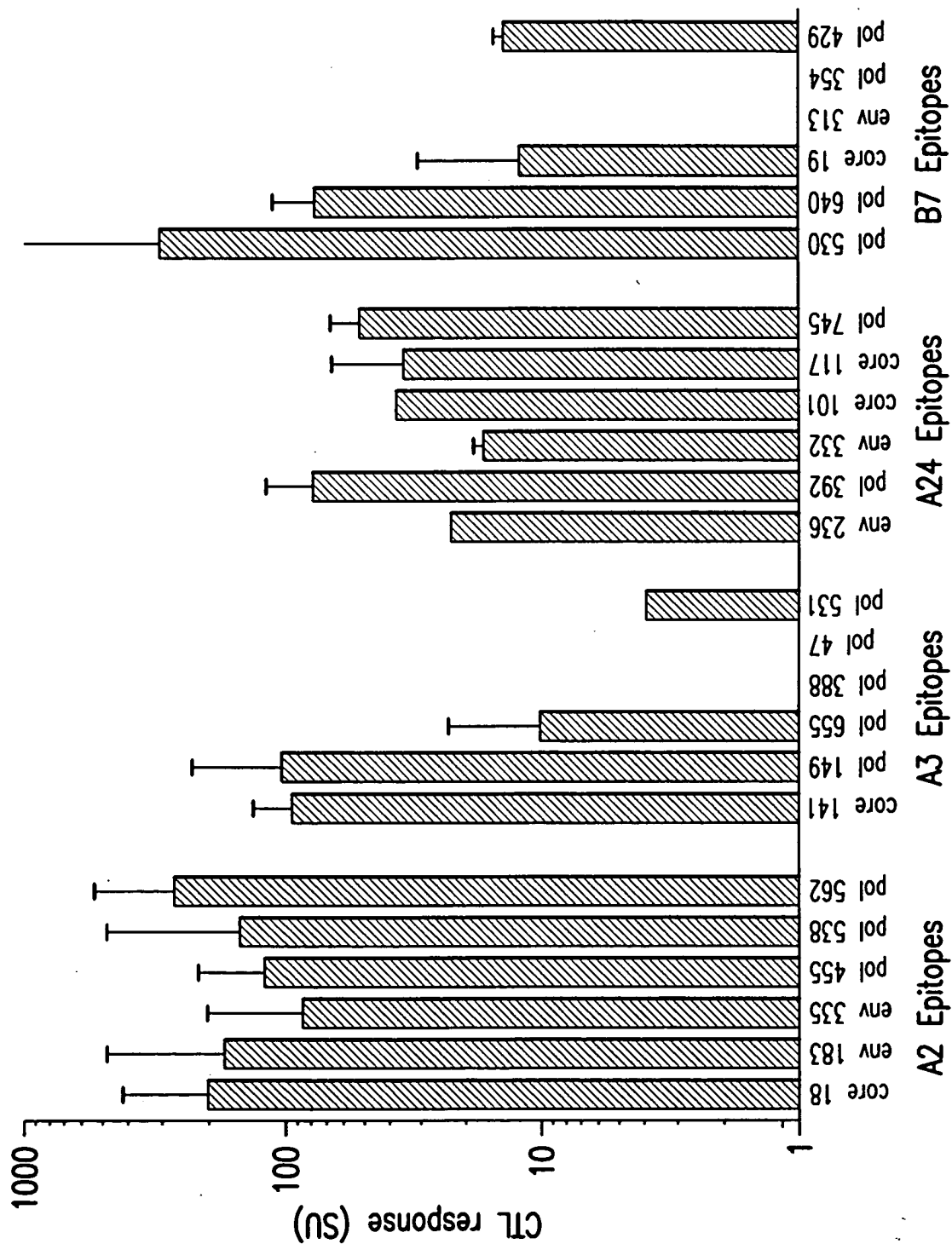


FIG.37A

88/90

GCR-3697 Immunogenicity Data

HLA Supertype	Epitope	CTL response (SU)				CT Pre-treatment GeoMean X/÷
		2 x PVP Immunization		CT		
		Freq.	GeoMean X/÷	Freq.	GeoMean X/÷	
HLA-A2	core 18	12/12	199.3	4/4	288.9	1.3
	env 183	12/12	171.2	4/4	401.2	1.4
	env 335	12/12	86.4	4/4	153.6	1.7
	pol 455	12/12	120.4	4/4	411.3	1.8
	pol 538	12/12	149.9	4/4	148.1	2.2
	pol 562	12/12	266.2	4/4	353.3	1.5
HLA-A3	core 141	6/6	94.4	12/12	167.6	1.4
	pol 149	6/6	103	12/12	386.7	1.5
	pol 655	5/6	10.1	12/12	108	3.6
	pol 388	0/6		0/12		
	pol 47	0/6		3/12	3.2	1.1
	pol 531	1/6	3.9	2/12	5.5	1
HLA-A24	env 236	1/6	22.6	2/11	23.4	1.2
	pol 392	5/6	78.1	10/11	54.8	2.2
	env 332	2/6	16.7	3/11	25.6	1.6
	core 101	1/6	37	0/11		
	core 117	3/6	34.4	2/11	27.4	3
	pol 745	2/6	51.2	1/11	32.6	
HLA-B7	pol 530	6/6	292.4	3/6	177	1.3
	pol 640	4/6	76.5	5/7	104.6	1.8
	core 19	3/6	12	2/7	8.8	1.6
	env 313	0/6	0	6/6	323.1	2.9
	pol 354	0/6	0	4/6	351.5	3.2
	pol 429	2/6	13.7	1/6	1.4	

FIG.37B

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☒ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.